

# FIGURE 1

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R35464 GGCCGGGTCG TTTCTCGCCT GGCTGGGATC GCTGCTCCTC TCTGGGGTCC 50
ORF    P G R F S P G W D R C S S L G S 16

R35464 TGGCCGGCCG ACCGAGAAGC CAGCATCCAC GACTTCTGCC TGGTGTGAA 100
ORF    W P A D R E R S I H D F C L V S K 33

R35464 GGTGGTGGGC AGATTCCGGG CCTCCATGCC TAGGTGGTGG TACAATGTCA 150
ORF    V V G R E R A S M P R W W Y N V T 50

R35464 CTGACGGATC CTGCCAGCTG TTTGTGTATG GGGGCTGTGA CGGAAACAGC 200
ORF    D G S C Q L F V Y G G C D G N S 66

R35464 AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGTCAC 250
ORF    N N Y L T K E E C L K K C A T V T 83

R35464 AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATTCCT 300
ORF    E N A T G D L A T S R N A A D S S 100

R35464 CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CTTGAAGACC ACTTCAGCGA 350
ORF    V P S A P R R Q D S * R P L Q R 116

R35464 TATGTTTCAA NTATTGNAAG AATAATTGCA CCGNCAACGN ATT----- 393
ORF    Y V S * I * R I I A P * T * 130
  
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## KEY

R35464 = Nucleic acid sequence of EST R35464 (SEQ ID NO: 12)

ORF = EST R35464 Open Reading Frame Translation (SEQ ID NO: 13)

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FIGURE 2

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R74593	GCAATAATTA	CCTGACCAAG	GAGGAGTGCC	TCAAGAAATG	TGCCACTGTC	50
ORF	Q	*	L	P	D	Q
			G	V	P	Q
				E	M	C
				H	C	H
						17
R74593	ACAGAGAATG	CCACGGGTGA	CCTGGCCACC	AGCAGGAATG	CAGCGGATTC	100
ORF	R	E	C	H	G	*
			P	G	H	Q
				Q	E	C
				S	G	F
						33
R74593	CTCTGTCCCA	AGTCTCCCAG	AAGGCAGGAT	TCTGAAGACC	ACTCCAGCGA	150
ORF	L	C	P	K	S	P
			R	Q	D	S
				E	D	H
				S	S	D
						50
R74593	TATGTTCAAC	TATGAAGAAT	ACTGCACCGC	CAACGCAGTC	ACTGGGCCTT	200
ORF	M	F	N	Y	E	E
			Y	C	T	A
				N	A	V
				T	G	P
						C
						67
R74593	GCCGTGCATC	CTTCCCACGC	TGGTACTTTG	ACGTGGAGAG	GAACTCCTGC	250
ORF	R	A	S	F	P	R
			W	Y	F	D
				V	E	R
				N	S	C
						83
R74593	AATAACTTCA	TCTATGGAGG	CTGCCGGGGC	AATAAGAACA	GCTACCGCTC	300
ORF	N	N	F	I	Y	G
			G	C	R	G
				N	K	N
				S	Y	R
						S
						100
R74593	TGAGGAGGCC	TGCATGCTCC	GCTGCTTCCG	CCAGCAGGAG	AATCCTCCCC	350
ORF	E	E	A	C	M	L
			R	C	F	R
				Q	Q	E
				N	P	P
						L
						117
R74593	TGCCCCTTGG	CTCAAAGGTG	GTGGTTCTGG	CCGGGGCTGT	TTCGTGATGG	400
ORF	P	L	G	S	K	V
				V	V	L
				A	G	A
				V	S	*
						W
						133
R74593	TGTTGATCCT	TTTCCTGGGG	AGCNTCCATG	GTCTTACTGA	TTCCGGGTGG	450
ORF	C	*	S	F	S	W
			G	A	S	M
				V	L	L
				I	P	G
						G
						150
R74593	CAAGGAGGAA	CCAGGAGCGT	GCCCTGCGGA	NCGTCTGGAG	CTTCGGAGAT	500
ORF	K	E	E	P	G	A
			C	P	A	X
				R	L	E
				L	R	R
				*		
						167
R74593	GACAAGGGNT					510
ORF	Q	G				169

KEY

R74593 = Nucleic acid sequence of EST R74593 (SEQ ID NO: 14)

ORF = EST R74593 Open Reading Frame Translation (SEQ ID NO: 15)

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FIGURE 3

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R35464	GGCCGGGTCGT	TTCTCGCCTG	GCTGGGA-TC	GCTGCTCCTC	TCTGGGGTCC	50
N39798			TGGGANTC	GCTGCTCCTC	TCTGGGGTCC	28
H94519	GCNGCG-CGT	TNNTCGCNT-	GCTGGGA-TC	GCTGCACCTC	TCTGGGGTCC	47
R74593 corr.	-----	-----	-----	-----	-----	
Consensus	GGCCGGGTCGT	TTCTCGCCTG	GCTGGGA-TC	GCTGCTCCTC	TCTGGGGTCC	50
Translation	A G S F	L A W	L G S	L L L	S G V	-3
R35464	TGGCCGGCCG	ACCGAGAACG	CAGCATCCAC	GACTTCTGCC	TGGTGTGCGAA	100
N39798	TGG-CGGCCG	ACCGAGAACG	CAGCATCCAC	GACTTCTGCC	TGGTGTGCGAA	77
H94519	NGG-CGGCCG	ACCGAGAACG	CAGCATCCAC	GACTTCTGCC	TGGTGTGCGAA	96
R74593 corr.	-----	-----	-----	-----	-----	
Consensus	TGG-CGGCCG	ACCGAGAACG	CAGCATCCAC	GACTTCTGCC	TGGTGTGCGAA	99
Translation	L A A D	B E B	S I H	D E C L	V S K	15
R35464	GGTGGTGGGC	AGATTCCGGG	CCTCCATGCC	TAGGTGGTGG	TACAATGTCA	150
N39798	GGTGGTGGGC	AGATGCCGGG	CCTCCATGCC	TAGGTGGTGG	TACAATGTCA	127
H94519	GGTGGTGGGC	AGATGCCGGG	CCTCCATGCC	TAGGTGGTGG	TACAATGTCA	146
R74593 corr.	-----	-----	-----	-----	-----	
Consensus	GGTGGTGGGC	AGATGCCGGG	CCTCCATGCC	TAGGTGGTGG	TACAATGTCA	149
Translation	V V G	B C B A	S M R	B H H	X N V T	32
R35464	CTGACGGATC	CTGCCAGCTG	TTTGTGTATG	GGGGCTGTGA	CGGAAACAGC	200
N39798	CTGACGGATC	CTGCCAGCTG	TTTGTGTATG	GGGGCTGTGA	CGGAAACAGC	177
H94519	CTGACGGATC	CTGCCAGCTG	TTTGTGTATG	GGGGCTGTGA	CGGAAACAGC	196
R74593 corr.	-----	-----	-----	-----	-----GC	2
Consensus	CTGACGGATC	CTGCCAGCTG	TTTGTGTATG	GGGGCTGTGA	CGGAAACAGC	199
Translation	D G S	C Q L	E V Y G	G C D	G N S	48
R35464	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTCAC	250
N39798	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTCAC	227
H94519	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTCAC	246
R74593 corr.	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTCAC	52
Consensus	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTCAC	249
Translation	N N Y L	T K E	E C L	K K C A	T V T	65
R35464	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCCT	300
N39798	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCCT	277
H94519	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCCT	296
R74593 corr.	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCCT	102
Consensus	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCCT	299
Translation	E N A	T G D L	A T S	R N A	A D S S	92
R35464	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CTTGAAGACC	ACTTCAGCGA	350
N39798	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CT-GAAGACC	ACTCCAGCGA	326
H94519	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CT-GAAGACC	ACTCCAGCGA	345
R74593 corr.	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CT-GAAGACC	ACTCCAGCGA	151
Consensus	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CT-GAAGACC	ACTCCAGCGA	348
Translation	V P S	A P R	R Q D S	E D H	S S D	98
R35464	TATGTTTCAA	NTATTGNAAG	AATAATTGCA	CCGNCAACGN	ATT-----	393
N39798	TATGTT-CAA	CTA-TG-AAG	AATACT-GCA	CCGCCAACGC	AGTCACTGGG	372
H94519	TATGTT-CAA	CTA-TG-AAG	AATACTGGCA	CCGCCAACGC	ATTCACTGGG	392
R74593 corr.	TATGTT-CAA	CTA-TG-AAG	AATACT-GCA	CCGCCAACGC	AGTCACTGGG	197
Consensus	TATGTT-CAA	CTA-TG-AAG	AATACT-GCA	CCGCCAACGC	AGTCACTGGG	394
Translation	M F N	Y E E	Y C T	A N A	V T G	113

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FIGURE 3 (CONT)

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R35464	-----	-----	-----	-----	-----	
N39798	CCTTGC-GTG	GAATCCTTTC	CCACGCTGGN	AATTTNGACG	TTGAGAAGGA	421
H94519	CCT-GC-GTG	-CATCCTT-C	CCACGCTGGT	ACTTT-GNCG	-----	427
R74593 corr.	CCTTGCCGTG	-CATCCTT-C	CCACGCTGGT	ACTTT-GACG	TGGAGA-GGA	243
Consensus	CCTTGCCGTG	-CATCCTT-C	CCACGCTGGT	ACTTT-GACG	TGGAGA-GGA	440
Translation	P C R A	S F	P R W Y	F D V	E R N	129

R35464	-----	-----	-----	-----	-----	
N39798	AC-----	-----	-----	-----	-----	423
H94519	-----	-----	-----	-----	-----	
R74593 corr.	ACTCCTGCAA	TAACTTCATC	TATGGAGGCT	GCCGGGGCAA	TAAGAACAGC	293
Consensus	ACTCCTGCAA	TAACTTCATC	TATGGAGGCT	GCCGGGGCAA	TAAGAACAGC	490
Translation	S C N	N F I	Y G G C	R G N	K N S	145

R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	TACCGCTCTG	AGGAGGCCTG	CATGCTCCGC	TGCTTCCGCC	AGCAGGAGAA	343
Consensus	TACCGCTCTG	AGGAGGCCTG	CATGCTCCGC	TGCTTCCGCC	AGCAGGAGAA	540
Translation	Y R S E	E A C	M L R	C F R Q	Q E N	162

R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	TCCTCCCCTG	CCCCTTGGCT	CAAAGGTGGT	GGTTCTGGCC	GGGGCTGTTT	393
Consensus	TCCTCCCCTG	CCCCTTGGCT	CAAAGGTGGT	GGTTCTGGCC	GGGGCTGTTT	590
Translation	P P L	P L G S	K V V	V L A	G A V S	179

R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	CGTGATGGTG	TTGATCCTTT	TCCTGGGGAG	CNTCCATGGT	CTTACTGATT	443
Consensus	CGTGATGGTG	TTGATCCTTT	TCCTGGGGAG	CNTCCATGGT	CTTACTGATT	640
Translation	* W C	* S F	S W G A	S M V	L L I	195

R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	CCGGGTGGCA	AGGAGGAACC	AGGAGCGTGC	CCTGCGGANC	GTCTGGAGCT	493
Consensus	CCGGGTGGCA	AGGAGGAACC	AGGAGCGTGC	CCTGCGGANC	<u>GTCTGGAGCT</u>	690
Translation	P G G K	E E P	G A C	P A * R	L E L	212

R35464	-----	-----				
N39798	-----	-----				
H94519	-----	-----				
R74593 corr.	TCGGAGATGA	CAAGGGNT				511
Consensus	<u>TCGGAGATGA</u>	CAAGGGNT				708
Translation	R R *	Q G				217

## KEY

R35464 = Nucleic acid sequence of EST R35464 (SEQ ID NO.: 12)

N39798 = Nucleic acid sequence of EST N39798 (SEQ ID NO.: 17)

H94519 = Nucleic acid sequence of EST H94519 (SEQ ID NO.: 16)

R74593 corr. = Corrected version of (SEQ ID NO.: 14) G at b.p. 114

Consensus = Nucleic acid sequence for human bikunin (SEQ ID NO.: 9)

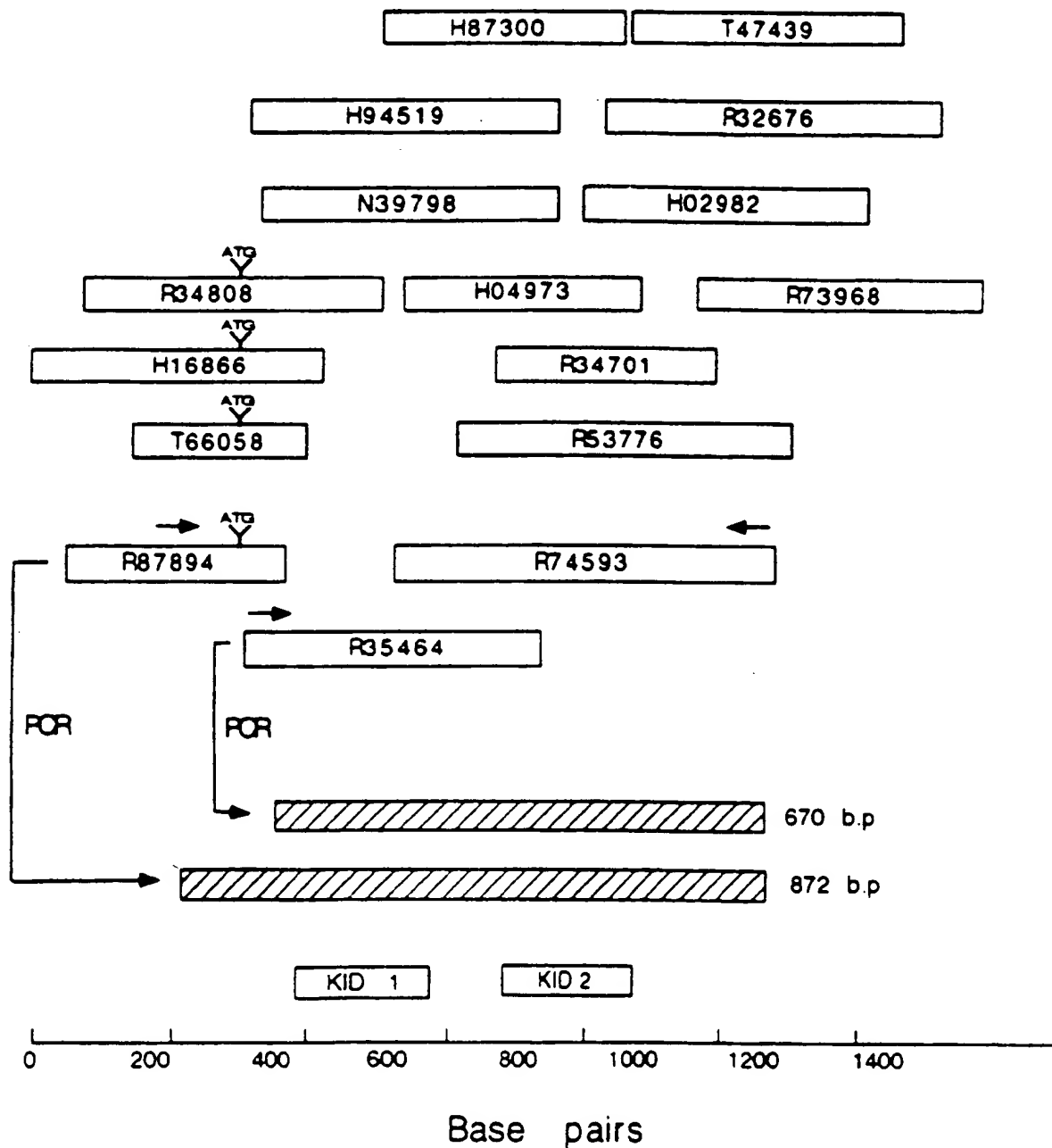
Translation = Amino acid Translation of Consensus (SEQ ID NO.: 10)

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Figure 4 A.

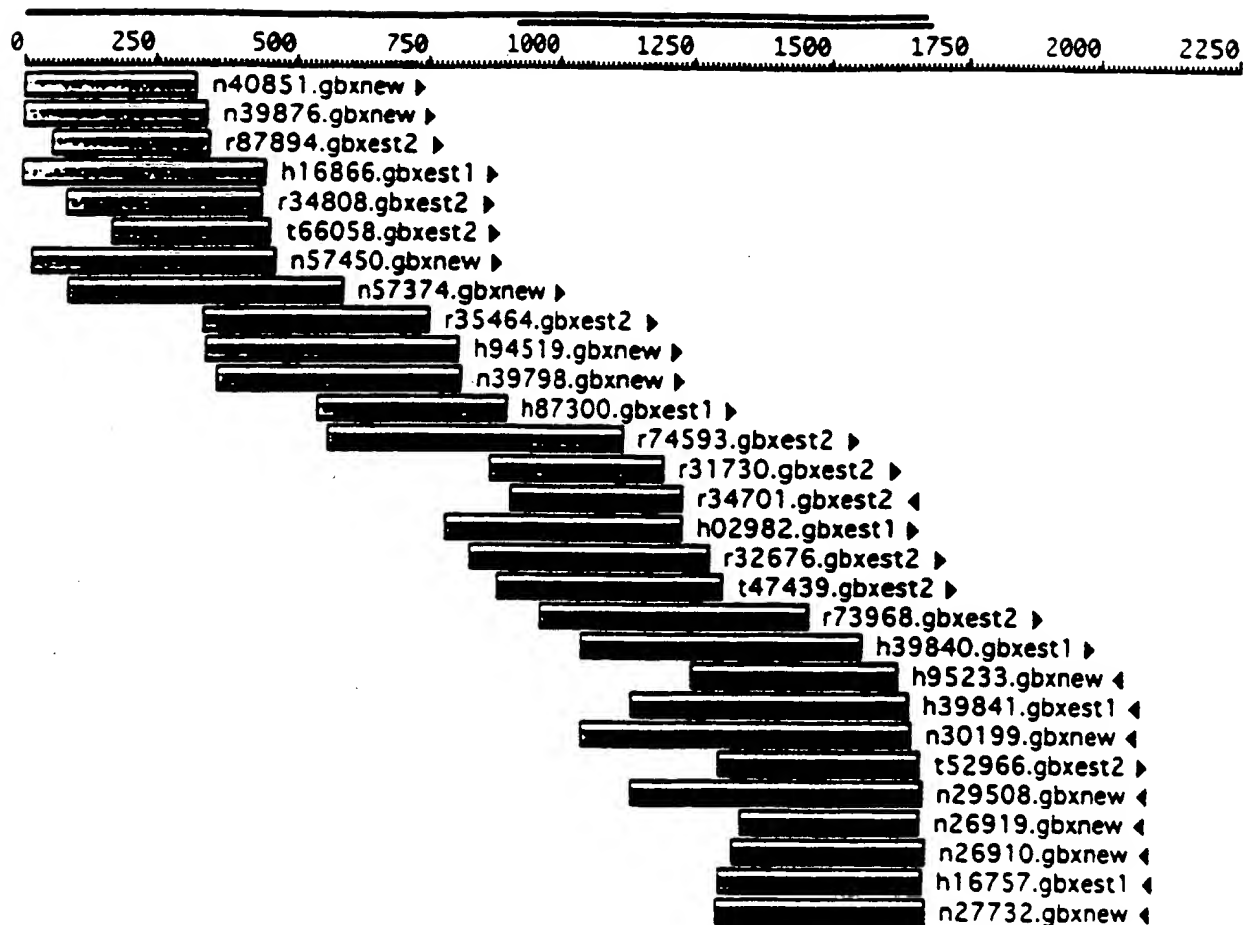
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Schematic depicting the overlap of ESTs bearing homology to the cDNA sequence encoding placental bikunin



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Figure 4B



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Figure 4C

	1		50
Bikunin	.....GCCA CCTCCGCGCG TTGGGAGGTG TAGCGCGGCT CTGAACGCGT		
N40851	.....GCCA CCTCCGCGCG TTGGGAGGTG TAGCGCGGCT CTGAACGCGT		
N39876	.....GCCA CCTCCGCGCG TTGGGAGGTG TAGCGCGGCT CTGAACGCGT		
R87894	.....		
H16866	.....GGCGA CCTCCGCGCG TTGGGAGGTG TAGCGCG.CT CTGAACGGGN		
R34808	.....		
T66058	.....		
N57450	.....T TAGCGCGGCT CTGAACGCNA		
N57374	.....		
R35464	.....		
H94519	.....		
N39798	.....		
H87300	.....		
R74593	.....		
R31730	.....		
R34701	.....		
H02982	.....		
R32676	.....		
T47439	.....		
R73968	.....		
H39840	.....		
H95233	.....		
H39841	.....		
N30199	.....		
T52966	.....		
N29508	.....		
N26919	.....		
N26910	.....		
H16757	.....		
N27732	.....		

BB2222T"ET6BT260

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Figure 4C (Con't)

	5:	100
Bikunin	GNA GGGCCG TTGAGTGTCC CAGGCGGCCA GGGCCGAGT GAGGAGCAGA	
N40851	NGAGNGGCCG TTGAGTGTCC CAGGCGGCCA GGGCCGAGT GAGGAGCAGA	
N39876	GCA.GGGCCG TTGAGTGTCC CAGGCGGCCA GGGCCGAGT GAGGAGCAGA	
R87894	..... TTGAGTGTNG NAGGCGGCCA GGGCCGAGT GAGGAGCAGA	
H16866	..ANGGCCG TTGAGTGTCC CAGGCGGC.A GGCEN.GAGT GAGGAGCAGA	
R34808	.....	.....G GAGGAGCAGA
T66058	.....	.....
N57450	GAAGNGGCCG TTGAGTGTCC CAGGCGGCCA GGGCCGAGT GAGGAGCAGA	
N57374	.....	.....AGA
R35464	.....	.....
H94519	.....	.....
N39798	.....	.....
H87300	.....	.....
R74593	.....	.....
R31730	.....	.....
R34701	.....	.....
HC2982	.....	.....
R32676	.....	.....
T47439	.....	.....
R73968	.....	.....
H39840	.....	.....
H95233	.....	.....
H39841	.....	.....
N30199	.....	.....
T52966	.....	.....
N29508	.....	.....
N26919	.....	.....
N26910	.....	.....
H16757	.....	.....
N27732	.....	.....

B16222T" E16B1260



**00000000000000000000000000000000**

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: 50

Bikunin	CCCAGGCATC	GCGCGCCGAG	AAGNC.GGGC	GTCCCCACAC	TGAAGGTCCG
N40851	CCCAGGCATC	GCGCGCCGAG	AAGNC.GGGC	GTCCCCACAC	TGAAGGTCCG
N39876	CCCAGGCATC	GCGCGCCGAG	AAGNC.GGGC	NTCCCCACAC	TGAAGGTCCG
R87894	CCCAGGCATC	GCGCGCCGAG	AAGGCCGGGC	GTCCCCACAC	TGAAGGTCCG
H16866	CCCAGGCATC	GCGCGCCGAG	AAGNC.GGGC	GTCCCCACAC	TGAAGGTCCG
R34808	CCCAGGCATC	GCGCGCCGAG	AAGNC.GGGC	GTCCCCACAC	TGAAGGTCCG
T66058	.....	.....	.....	.....	.....
N57450	CCCAGGCATC	GCGCGCCGAG	AAGNC.GGGC	GTCCCCACAC	TGAAGGTCCG
N57374	CCCAGGCATC	GCGCGCCGAG	AAGNC.GGGC	GTCCCCACAC	TGAAGGTCCG
R35464	.....	.....	.....	.....	.....
H94519	.....	.....	.....	.....	.....
N39798	.....	.....	.....	.....	.....
H87300	.....	.....	.....	.....	.....
R74593	.....	.....	.....	.....	.....
R31730	.....	.....	.....	.....	.....
R34701	.....	.....	.....	.....	.....
H02982	.....	.....	.....	.....	.....
R32676	.....	.....	.....	.....	.....
T47439	.....	.....	.....	.....	.....
R73968	.....	.....	.....	.....	.....
H39840	.....	.....	.....	.....	.....
H95233	.....	.....	.....	.....	.....
H39841	.....	.....	.....	.....	.....
N30199	.....	.....	.....	.....	.....
T52966	.....	.....	.....	.....	.....
N29508	.....	.....	.....	.....	.....
N26919	.....	.....	.....	.....	.....
N26910	.....	.....	.....	.....	.....
H16757	.....	.....	.....	.....	.....
N27732	.....	.....	.....	.....	.....

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Figure 4C (Con't)

	151				200
Bikunin	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
N40851	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
N39876	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
R87894	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
H16866	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACG.T	CCCGGAGCN.
R34808	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
T66058	.....	.....	.....	...GGACCCT	CCCGGAGCGT
N57450	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
N57374	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
R35464	.....	.....	.....	.....	.....
H94519	.....	.....	.....	.....	.....
N39798	.....	.....	.....	.....	.....
H87300	.....	.....	.....	.....	.....
R74593	.....	.....	.....	.....	.....
R31730	.....	.....	.....	.....	.....
R34701	.....	.....	.....	.....	.....
H02982	.....	.....	.....	.....	.....
R32676	.....	.....	.....	.....	.....
T47439	.....	.....	.....	.....	.....
R73968	.....	.....	.....	.....	.....
H39840	.....	.....	.....	.....	.....
H95233	.....	.....	.....	.....	.....
H39841	.....	.....	.....	.....	.....
N30199	.....	.....	.....	.....	.....
T52966	.....	.....	.....	.....	.....
N29508	.....	.....	.....	.....	.....
N26919	.....	.....	.....	.....	.....
N26910	.....	.....	.....	.....	.....
H16757	.....	.....	.....	.....	.....
N27732	.....	.....	.....	.....	.....

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Figure 4C (Con't)

	201	250
Bikunin	CGGCACCTGA ACGCGAGGCG CTCCATTGCG CGTGCGTTTG	.AGGGGGCTTC
N40851	CGGCACCTGA ACGCGAGGCG CTCCATTGCG CGTGCGTNTG	.AGGGGGCTTC
N39876	CGGCACCTGA ACGCGAGGCG CTCCATTGCG CGTGCGTTTG	.AGGGGGCTTC
R87894	CGGCACCTGA ACGCGAGGCG CTCCATTGCG CGTGCGTTTG	.AGGGGGCTTC
H16866	.GGCACCTGA ACGCGAGGCG CTCCATTGCG CGTGCGTTTG	.AGGGGGCTTC
R34808	CGGCACCTGA ACGCGAGGCG CTCCATTGCG CGTGCGTNTG	GAGGGGGCTTC
T66058	CGGCACCTGA ACGCGAGGCG CTCCATTGCG .GTGCGTGTG	NAGGGGGCTTC
N57450	CGGCACCTGA ACGCGAGGCG CTCCATTGCG CGTGCGTTTG	.AGGGGGCTTC
N57374	CGGCACCTGA ACGCGAGGCG CTCCATTGCG CGTGCGTTTG	.AGGGGGCTTC
R35464	.....	.....
H94519	.....	.....
N39798	.....	.....
H87300	.....	.....
R74593	.....	.....
R31730	.....	.....
R34701	.....	.....
H02982	.....	.....
R32676	.....	.....
T47439	.....	.....
R73968	.....	.....
H39840	.....	.....
H95233	.....	.....
H39841	.....	.....
N30199	.....	.....
T52966	.....	.....
N29508	.....	.....
N26919	.....	.....
N26910	.....	.....
H16757	.....	.....
N27732	.....	.....

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Figur 4C (C n't)

	251	300
Bikunin	CCGCACCT G ATCGCGAGAC CCCAACGGCT GGTGG CGTC GC TG CCGG	
N40851	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTGG.CGTC GCCTG.CCGG	
N39876	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTGG.CGTC GCCTG.CCGG	
R87894	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTNG.CGTC GC.TN.CCGG	
H16866	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTNG.CGTC GC.TGGCGCG	
R34808	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTGGGGCTG GC.TG.CCGG	
T66058	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTGG.CGTC GC.TG.CCGG	
N57450	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTGG.CGTC GCCTG.CCGG	
N57374	CCGGAACTTG ATCGCGAGAC CCCAACGGCT GGTGG.CGTC GC.TG.CCGG	
R35464	.....	
H94519	.....	
N39798	.....	
H87300	.....	
R74593	.....	
R31730	.....	
R34701	.....	
H02982	.....	
R32676	.....	
T47439	.....	
R73968	.....	
H39840	.....	
H95233	.....	
H39841	.....	
N30199	.....	
T52966	.....	
N29508	.....	
N26919	.....	
N26910	.....	
H16757	.....	
N27732	.....	

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Figure 4C (C n't)

	30:		350
Bikunin	TC TCGGCTG AGCT GGCCA TGGCGCANT GTTGC GGGC T GAGGC GC		
N40851	TC.TCGGCTG AGCT.GGNCA TGTCG		
N39876	TC.TCGGCTG AGCT.GGCCA TGGCGCACT. G.TCGCGNGC T.GAGGC.G		
R87894	TC.TCGGCTG AGCTTGGCCA TGGCGCANT. GTTNC.GGGC T.NAGGC.GG		
H16866	TTCTCGGCTG AGCT.GGCCA TGGCGCANT. GTTGC.GNGC T.GAGGC.GG		
R34808	TCTTCGGCTG AGCTGGGCCA TGGCGCANTT GTTGC.GGGC T.GAGGC.GG		
T66058	TC.TCGGCTG AGCT.GGCCA TGGCGCANT. GTTGC.GNGC T.GAGGC.GG		
N57450	TC.TCGGCTG AGCT.GGCCA TGGCGCANT. GGTGC.GGGC TTGAGGC.GG		
N57374	TCCTCGGCTG AGCT.GGCCA TGGCGCANT. GGTGCCGNGC T.GAGGCCGG		
R35464	.....	....GGCCGG	
H94519	.....		
N39798	.....		
H87300	.....		
R74593	.....		
R31730	.....		
R34701	.....		
H02982	.....		
R32676	.....		
T47439	.....		
R73968	.....		
H39840	.....		
H95233	.....		
H39841	.....		
N30199	.....		
T52966	.....		
N29508	.....		
N26919	.....		
N26910	.....		
H16757	.....		
N27732	.....		

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Figure 4C (Con't)

35: 400

Bikunin AC GG CG TTTCTCG CC TGCTGGG A TCGCT GC T CCTCTCT  
R87894 ACG.

H16866 AC..CGNCST TTTCTCTCG. CCTTGCTGGG ATTGCTTGC TTCTNTCTG  
R34808 ACGCGGNCG. .TTTTTTCGN CCTTGCTGGG ATTGCTTGC TTCTNTCTN  
T66058 ...CGGNCG. .TTTTCTCG. CC.TGCTGGG A.TCGCT.GC T.CCTCTCT.  
N57450 ANN.NGCCG. .TTTTCTCG. CC.TGCTGGG A.TCGCT.GC T.CCTCTCT.  
N57374 AG..GGCCGG .TTTTCTCG. CCTTGCTGGG A.TCGCT.GC T.CCTCTCTG  
R35464 .....GTCTG. .TTTTCTCG. CCTTGCTGGG A.TCGCT.GC T.CCTCTCT.  
H94519 .GCNGCGCG. .TTNNTCG. CN.TGCTGGG A.TCGCT.GC A.CCTCTCT.  
N39798 .....CTGGG ANTGGCT.GC T.CCTCTCT.  
H87300 .....  
R74593 .....  
R31730 .....  
R34701 .....  
H02982 .....  
R32676 .....  
T47439 .....  
R73968 .....  
H39840 .....  
H95233 .....  
H39841 .....  
N30199 .....  
T52966 .....  
N29508 .....  
N26919 .....  
N26910 .....  
H16757 .....  
N27732 .....

001691-2222

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Figure 4C (C n't)

	401	450
Bikurin	GGGG TCCTG G CGGCCGA CCGA GAACG CA GCA TCC ACGACTT CT	
H16866	GGGGTTCTG GG.CGGCCGA CCGA.GAACG CA.GCA.TCC AAGAATTTT	
R34808	GGGGTTC.TG GGGNGGCCGA NCGA.GAACG CAAGCA.TTC ACCA.TTT	
T66058	GGGG.TCCTG G..CGGCCGA CCGA.GAACG CA.GCA.TCC ACGANTT.CT	
N57450	GGGG.TCCTG G..CGGCCGA CCGA.GAACG CA.GCA.TCC ACGACTT.CT	
N57374	GGGG.TCCTG G..CGGCCGA NCGAAGAANG CA.GCAATCC ANGAATTNC	
R35464	GGGG.TCCTG G.CGGCCGA CCGA.GAACG CA.GCA.TCC ACGACTT.CT	
H94519	GGGG.TCGNG G..CGGCCGA CCGA.GAACG CA.GCA.TCC ACGACTT.CT	
N39798	GGGG.TCCTG G..CGGCCGA CCGA.GAACG CA.GCA.TCC ACGACTT.CT	
H87300	.....	
R74593	.....	
R31730	.....	
R34701	.....	
H02982	.....	
R32676	.....	
T47439	.....	
R73968	.....	
H39840	.....	
H95233	.....	
H39841	.....	
N30199	.....	
T52966	.....	
N29508	.....	
N26919	.....	
N26910	.....	
H16757	.....	
N27732	.....	

BBBCT"CTBTEBO

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Figure 4C (C n't)

	451		500
Bikunin	GCCTGGTGT	CGAAGGT GG	TGGGCAGATG CCGGG CCTC CATGCCTA G
H16866	GCC		
T66058	TCCTGGTGT	CGAAGG	
N57450	GCCTGGTGT	CGAAGGT GG	TGGGCAG
N57374	GCCTGGTGT	CGAAGTTGG	TGGGCANATT CCGGGCCTT CATGNCTAAG
R35464	GCCTGGTGT	CGAAGGT GG	TGGGCAGATT CCGGG.CCTC CATGCCTA.G
H94519	GCCTGGTGT	CGAAGGT GG	TGGGCAGATG CCGGG.CCTC CATGCCTA.G
N39798	GCCTGGTGT	CGAAGGT GG	TGGGCAGATG CCGGG.CCTC CATGCCTA.G
H87300	.....	.....	.....
R74593	.....	.....	.....
R31730	.....	.....	.....
R34701	.....	.....	.....
H02982	.....	.....	.....
R32676	.....	.....	.....
T47439	.....	.....	.....
R73968	.....	.....	.....
H39840	.....	.....	.....
H95233	.....	.....	.....
H39841	.....	.....	.....
N30199	.....	.....	.....
T52966	.....	.....	.....
N29508	.....	.....	.....
N26919	.....	.....	.....
N26910	.....	.....	.....
H16757	.....	.....	.....
N27732	.....	.....	.....

362221 " E F 68 F 260



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Figure 4C (Con't)

	501		550
Bikunin	G TGGT GGT ACAATGTCAC TGACGGATCC TGCCAGCTGT TTGTGT ATG		
N57374	GTTGGTTGGT ANAATGTNAA TTAANGATTC TTGCAACTGT TTGTGTNATT		
R35464	G.TGGT.GGT ACAATGTCAC TGACGGATCC TGCCAGCTGT TTGTGT.ATG		
H94519	G.TGGT.GGT ACAATGTCAC TGACGGATCC TGCCAGCTGT TTGTGT.ATG		
N39798	G.TGGT.GGT ACAATGTCAC TGACGGATCC TGCCAGCTGT TTGTGT.ATG		
H87300	.....		
R74593	.....		
R31730	.....		
R34701	.....		
H02982	.....		
R32676	.....		
T47439	.....		
R73968	.....		
H39840	.....		
H95233	.....		
H39841	.....		
N30199	.....		
T52966	.....		
N29508	.....		
N26919	.....		
N26910	.....		
H16757	.....		
N27732	.....		

	551		600
Bikunin	GGGGCTGTGA CGGAAACA GCAATAATTA CCTGACCAAG GA GGAGTGC		
N57374	GGGGCTNTTA AACCGAAANA .CAATAATNA CCTGACCAAA GAAGNAAT..		
R35464	GGGGCTGTGA ..CGGAAACA GCAATAATTA CCTGACCAAG GA.GGAGTGC		
H94519	GGGGCTGTGA ..CGGAAACA GCAATAATTA CCTGACCAAG GA.GGAGTGC		
N39798	GGGGCTGTGA ..CGGAAACA GCAATAATTA CCTGACCAAG GA.GGAGTGC		
H87300	GATTGGGCAC AGGGGAAACA GCAATAATTA CCTGACCAAG GA.GGAGTNC		
R74593	..... GCAATAATTA CCTGACCAAG GA.GGAGTGC		
R31730	.....		
R34701	.....		
H02982	.....		
R32676	.....		
T47439	.....		
R73968	.....		
H39840	.....		
H95233	.....		
H39841	.....		
N30199	.....		
T52966	.....		
N29508	.....		
N26919	.....		
N26910	.....		
H16757	.....		
N27732	.....		

Bikunin "CTGTGTA"

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Figure 4C (Con't)

	601				650
Bikunin	CTCAAGAAAT GTGCCACTGT CACAGAGAAT GCCACGGGTG ACCTGGCCAC				
R35464	CTCAAGAAAT GTGCCACTGT CACAGAGAAT GCCACGGGTG ACCTGGCCAC				
H94519	CTCAAGAAAT GTGCCACTGT CACAGAGAAT GCCACGGGTG ACCTGGCCAC				
N39798	CTCAAGAAAT GTGCCACTGT CACAGAGAAT GCCACGGGTG ACCTGGCCAC				
H87300	CTCAAGAAAT GTGCCACTGT CACAGAGAAT GCCACGGGTG ACCTGGCCAC				
R74593	CTCAAGAAAT GTGCCACTGT CACAGAGAAT GCCACGGGTG ACCTGGCCAC				
R31730	.....				
R34701	.....				
H02982	.....				
R32676	.....				
T47439	.....				
R73968	.....				
H39840	.....				
H95233	.....				
H39841	.....				
N30199	.....				
T52966	.....				
N29508	.....				
N26919	.....				
N26910	.....				
H16757	.....				
N27732	.....				
	651				700
Bikunin	CAGCAGGAAT GCAGCGGATT CCTCTGTCCC AAGTGCTCCC AGAAGGCAGG				
R35464	CAGCAGGAAT GCAGCGGATT CCTCTGTCCC AAGTGCTCCC AGAAGGCAGG				
H94519	CAGCAGGAAT GCAGCGGATT CCTCTGTCCC AAGTGCTCCC AGAAGGCAGG				
N39798	CAGCAGGAAT GCAGCGGATT CCTCTGTCCC AAGTGCTCCC AGAAGGCAGG				
H87300	CAGCAGGAAT GCAGCGGATT CCTCTGTCCC AAGTGCTCCC AGAAGGCAGG				
R74593	CAGCAGGAAT GCAGCGGATT CCTCTGTCCC AAGTGCTCCC AGAAGGCAGG				
R31730	.....				
R34701	.....				
H02982	.....				
R32676	.....				
T47439	.....				
R73968	.....				
H39840	.....				
H95233	.....				
H39841	.....				
N30199	.....				
T52966	.....				
N29508	.....				
N26919	.....				
N26910	.....				
H16757	.....				
N27732	.....				

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Figure 4C (C n't)

	701	750
Bikunin	ATTCT GAAG ACCACTCCAG CGATATGTT	CAACTAT G AAGAATACTG
R35464	ATTCTTGAAG ACCACTTCAG CGATATGTTT	CAANTATTGN AAGAATAATT
H94519	ATTCT.GAAG ACCACTCCAG CGATATGTT.	CAACTAT..G AAGAATACTG
N39798	ATTCT.GAAG ACCACTCCAG CGATATGTT.	CAACTAT..G AAGAATACTG
H87300	ATTCT.GAAG ACCACTCCAG CGATATGTT.	CAACTAT..G AAGAATACTG
R74593	ATTCT.GAAG ACCACTCCAG CGATATGTT.	CAACTAT..G AAGAATACTG
R31730	.....	.....
R34701	.....	.....
H02982	.....	.....
R32676	.....	.....
T47439	.....	.....
R73968	.....	.....
H39840	.....	.....
H95233	.....	.....
H39841	.....	.....
N30199	.....	.....
T52966	.....	.....
N29508	.....	.....
N26919	.....	.....
N26910	.....	.....
H16757	.....	.....
N27732	.....	.....
	751	800
Bikunin	CACCGCCAA CGCAGT CAC TGGGCC TTG CCGTG CAT	CCTT CCCAC
R35464	GCACCGNCAA CGNATT	
H94519	GCACCGCCAA CGCATT.CAC TGGGCC..TG C.GTG.CAT.	CCTT.CCCAC
N39798	.CACCGCCAA CGCAGT.CAC TGGGGCCTTG C.GTGGAAT.	CCTTCCCAC
H87300	.CACCGCCAA CGCAGTNCAC TGGGCC.TTG C.GTGGCATN	CCTT.CCCAC
R74593	.CACCGCCAA CGCAGT.CAC TGGGCC.TTG CCGTG.CAT.	CCTT.CCCAC
R31730	.....	.....
R34701	.....	.....
H02982	.....	.....
R32676	.....	.....
T47439	.....	.....
R73968	.....	.....
H39840	.....	.....
H95233	.....	.....
H39841	.....	.....
N30199	.....	.....
T52966	.....	.....
N29508	.....	.....
N26919	.....	.....
N26910	.....	.....
H16757	.....	.....
N27732	.....	.....

352221" E T B F 260

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Figure 4C (C n't)

	801	850
Bikunin	GCTGGTACTT T GACGTGGA GA GGAAGTC CTG CAATAA CTTCATCTAT	
H94519	GCTGGTACTT T.GNCGT	
N39798	GCTGGNAATT TNGACGTTGA GAAGGAAC	
H87300	GCTNGTACTT T.GACGTGGA GA.GGAAGTC CTGGCAATAA CTTCATCTAT	
R74593	GCTGGTACTT T.GACGTGGA GA.GGAAGTC CTG.CAATAA CTTCATCTAT	
R31730	.....	
R34701	.....	
H02982	.....GA GA.GGAAGTC CTG.CAATAA CTTCATCTAT	
R32676	.....G ATTC..GGAA	
T47439	.....	
R73968	.....	
H39840	.....	
H95233	.....	
H39841	.....	
N30199	.....	
T52966	.....	
N29508	.....	
N26919	.....	
N26910	.....	
H16757	.....	
N27732	.....	

	851	900
Bikunin	GGAGGCT GC CGGGGCAAT AAGAACAG C TACCGCTC T GAGGAGGCCT	
H87300	GGAGGCTTGC CGGGGCAATN AAGAACAGNT TACCGCTCTT TAGGAGGCCT	
R74593	GGAGGCT.GC CGGGGCAAT. AAGAACAG.C TACCGCTC.T GAGGAGGCCT	
R31730	.....G.C TACCGCTC.T GAGGAGGCCT	
R34701	.....	
H02982	GGNGGCT.GC CGGGG.AAT. AAGAACA.NC TACCGCTC.T GAGGAGGCCT	
R32676	CGAGGA..GC CGGGGCAAT. AAGAACAG.C TACCGCTC.T GAGGAGGCCT	
T47439	.....NGGCCT	
R73968	.....	
H39840	.....	
H95233	.....	
H39841	.....	
N30199	.....	
T52966	.....	
N29508	.....	
N26919	.....	
N26910	.....	
H16757	.....	
N27732	.....	

GGAGGCT " E F G T 260

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Figure 4C (Con't)

	901	950
Bikunin	GCA TGCTC CGGTGCTTCC GC	CA GCAGGA
H87300	.GCA.T....	
R74593	.GCA.TGCTC CGGTGCTTCC GC.....	.CA.GCAGGA
R31730	.GCA.TGCTC CGGTGCTTCC GC.....	.CA.GCAGGA
R34701	.....TTCC GC.....	.CAAGCAGGA
H02982	.GCG.TGCTC CGGTGCTTCC GCTGTGTSTT CTCTTCCAGG	CCA.GCAGGA
R32676	.GCA.TGCTC CGGTGCTTCC GC.....	.CA.GCAGGA
T47439	TGCAGTGCTC CGGTGCTTCC GC.....	.CA.GCAGGA
R73968	.....	
H39840	.....	
H95233	.....	
H39841	.....	
N30199	.....	
T52966	.....	
N29508	.....	
N26919	.....	
N26910	.....	
H16757	.....	
N27732	.....	

	951	1000
Bikunin	GAA TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC	TGG CGGGGC
R74593	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC.	TGGCGGGGC
R31730	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC.	TGG.CGGGGC
R34701	AAANTCCTCC CCTCCCCCTT GGCTCAAAGG TGGTGGTTC	TGG.CGGGGC
H02982	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC.	TGG.CGGGGC
R32676	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC.	TGG.CGGGGC
T47439	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC.	TGG.CGGGGC
R73968	.....	....CGGGGC
H39840	.....	
H95233	.....	
H39841	.....	
N30199	.....	
T52966	.....	
N29508	.....	
N26919	.....	
N26910	.....	
H16757	.....	
N27732	.....	

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Figure 4C (Con't)

	1001		1050
Bikunin	TGTT CGTGA TGGTGTGAT CC T CTTC TGGG AGCCT CC ATGGTC		
R74593	TGTTTCGTGA TGGTGTGAT CCTT..TTCC TGGGGAGCCT CC.ATGGTCT		
R31730	TGTT.CGTGA TGGTGTGAT CC.T.CTTC TGGGGAGCCT CC.ATGGTC.		
R34701	TGTT.CGTGA TGGTGTGAT CCTCTCTTC CGGG.AGCCT CCCATGGTCC		
H02982	TGTT.CGTGA TGGTGTGAT CC.T.CTTC TGGG.AGCCT CC.ATGGTN.		
R32676	TGTT.CGTGA TGGTGTGAT CC.T.CTTC TGGG.AGCCT CC.ATGGTC.		
T47439	TGTT.CGTGA TGGTGTGAT CC.T.CTTC TGGG.AGCCT CC.ATGGTC.		
R73968	TGTT.CGTGA TGGTGTGAT CC.T.CTTC TGGG.AGCCT CC.ATGGTC.		
H39840	.....		
H95233	.....		
H39841	.....		
N30199	.....		
T52966	.....		
N29508	.....		
N26919	.....		
N26910	.....		
H16757	.....		
N27732	.....		

	1051		1100
Bikunin	TACC TGAT CCGGGTGGCA CGGAGG AAC C AGG AGCG TGGCCCTGCGC		
R74593	TACC.TGAT CCGGGTGGCA AGGAGG.AAC C.AGG.AGCG TGGCCCTGCGC		
R31730	TACC.TGAT CCGGGTGGCA CGGAGGGAAC C.AGGGAGCG TGGCCCTGCGC		
R34701	TACCCTGAT CCGGGTGGCA CGGAGG.AAC CCAGG.ANCG TGGCCCTGCGC		
H02982	TACC.TGAT CCGGGTNGCA CGGAGG.AAC C.AGGGAGCG TGGCCCTGCGN		
R32676	TACC.TGAT CCGGGTGGCA CGGAGG.AAC C.AGGGAGCG TGGCCCTGCGC		
T47439	TACC.TGAT CCGGGTNGCA CGGAGG.AAC C.AGG.AGCG TGGCCCTGCGC		
R73968	TACC.TGAT CCGGGTGGCA CGGAGG.AAC C.AGG.AGCG TGGCCCTGCGC		
H39840	.....GGG.AAC C.AGG.AGCG TGGCCCTGCGC		
H95233	.....		
H39841	.....		
N30199	.....GAGGAACC C.ANG.AGCT TGGCCCTGCGC		
T52966	.....		
N29508	.....		
N26919	.....		
N26910	.....		
H16757	.....		
N27732	.....		

0010913 12298

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## Figure 4C (Con't)

1101 1150

Bikunin ACCG TCT G GAGCTCCGGA GATGACAAGG AGCAGCTGG TGAAGAAC  
 R74593 ANCG.TCT.G GAGCTCCGGA GATGACAAGG GNT  
 R31730 ACCG.TCTGG GAGCTCCGGA GATGACAAGG GAGCAGCTGG GTGAAGAAC.  
 R34701 ACCG.TCT.G GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC.  
 H02982 ACCG.TCTNG GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC.  
 R32676 ACCG.TCTGG GAGCTCCGGA GATGACAAGG GAGCAGCTGG .TGAAGAAC.  
 T47439 ACCG.TCT.G GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC.  
 R73968 ACCG.TCT.G GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC.  
 H39840 ACCGGTCT.G GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC.  
 H95233 .....  
 H39841 .....  
 N30199 ACCG.TCT.G GAGCTCCGGA GATNACAANG .AGCAGCTGN .TGAAGAACC  
 T52966 .....  
 N29508 .....  
 N26919 .....  
 N26910 .....  
 H16757 .....  
 N27732 .....

1151 1200

Bikunin ACATATGT C CTGT GACCG CCCTGT CGC C AAGAGG A CT GGGGAA  
 R31730 ACATATGTTT CTGTTGACCG NCCTGTTCCG C.AAGAGG.A TTGGGGGAA.  
 R34701 ACATATGT.C CTGT.GACCG CCCTGT.CGC C.AAGAGG.A CT.GGGGAA.  
 H02982 ACATATGT.C CTGT.GACCG NCCTGTTCCG C.AAGAGG.A CTNGGGGGAAA  
 R32676 ACATATGTTT CTGTTGACCG CCCTGTTCCG C.AAGAGGGA NTGGGGGAA.  
 T47439 ACATATGT.C CTGT.GACCG CCCTGT.CGC C.AAGAGG.A CT.GGGGAA.  
 R73968 ACATATGT.C CTGT.GACCG CCCTGT.CGC C.AAGAGG.A CT.GGGGAA.  
 H39840 ACATATGT.C CTGT.GACCG CCCTGT.CGC C.AAGAGG.A CT.NGGGAA.  
 H95233 .....  
 H39841 .....C. CCCTGT.CGC CAAAAGG.A CT.GGGGAA.  
 N30199 ACATATGT.C CTGT.GACCG CCCTNT.CGC C.AAGAGG.A CT.GGGNAAA  
 T52966 .....  
 N29508 .....CC. CCCTNT.CGC C.AAGAGG.A CT.GGG.AA.  
 N26919 .....  
 N26910 .....  
 H16757 .....  
 N27732 .....

0021891412299

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Figure 4C (C n't)

1201 1250  
 Bikurin GGGAGGGG AGACTAT G TGT GA GCT TTTTTT AA A TAGA GG  
 R31730 .GGGAGGGG A  
 R34701 .GGGAGGGG. AGACTAT.G. TGT.GA.GCT TTTTTT..AA A.TA  
 H02982 GGGAGGGG. AGATTAT.G. TGTGA.GTT TTTTTT..AA ANTAG  
 R32676 GGGAGGGGG AGANTATTGT TGTGA.GNT TTTTTTAAA ATTAGGAGGG  
 T47439 .GGGAGGGG. AGACTAT.G. TGT.GA.GCT TTTTTT..AA A.TAGA..GG  
 R73968 .GGGAGGGG. AGACTAT.G. TGT.GA.GCT TTTTTT..AA A.TAGA..GG  
 H39840 .GGGAGGGG. AGACTAT.G. TGT.GA.GCT TTTTTT..AA A.TAGA..GG  
 H95233 .....  
 H39841 .GGGAGGGGA AAACNAT.G. TGT.GAACCT TTTTTT.AAA A.TAGA..GG  
 N30199 .GGGAGGNG. AGACTAT.G. TGT.AA.GCT TTTTTT..AA A.TAGA..GG  
 T52966 .....  
 N29508 .GGGAGGGG. AGACTA..G. TGT.GA.GCT TTTTTT..AA A.TAGA..GG  
 N26919 .....  
 N26910 .....  
 H16757 .....  
 N27732 .....

1251 1300  
 Bikurin GATTGACTC GCATTTC A GT GATC A TTAGGG CT GAGGTCTGTT  
 R32676 GNTTGANTTC GGNITTTNA GTTGATCCAT TTAGGGGGNT GAG  
 T47439 GATTGACTC..GGATTTC.A GT.GATC.A. TTAGGG..CT GAGGTCTNNT  
 R73968 GATTGACTC..GGATTTC.A GT.GATC.A. TTAGGG..CT GAGGTCTGTT  
 H39840 GATTGACTC..GGATTTC.A GT.GATC.A. TTAGGG..CT GAGGTCTGTT  
 H95233 .....A. TTAGGG..CT GAGGTCTGTT  
 H39841 GATTGACTC..GGATTTC.A GT.GATC.A. TTAGGG..CT GAGGTCTGTT  
 N30199 GATTGACTC..GGATTTCGA GT.GATC.A. TTAGGG..CT GAGGTCTGTT  
 T52966 .....  
 N29508 GATTGACTC..GGATTTC.A GT.GATCNA. TTAGGG..CT GAGGTCTGTT  
 N26919 .....  
 N26910 .....  
 H16757 .....  
 N27732 .....

1301 1350  
 Bikurin TCTCTGGGAG GTAGGACGGC TGCTTCC TG G TC TGGCA GGGATGGG  
 T47439 TCTCTNGGAG GTAGGACGA  
 R73968 TCTCTGGGAG GTAGGACGGC TGCTTCC TG GGTCTTGGCA .GGGATGGG  
 H39840 TCTCTGGGAG GTAGGACGGC TGCTTCC TG G.TC.TGGCA .GGGATGGG.  
 H95233 NCTCTGGGAG NTAGGACGGC TGCTTCTGTS G.TC.TGGCA .GGGATGGG.  
 H39841 TCTCTGGGAG GTAGGACGGC TGCTTCTGTS G.TC.TGGCA .GGGATGGG.  
 N30199 TCTCTGGGAG GTAGGACGGC TGCTTCC TG G.TC.TGGCA .GGGATGGG.  
 T52966 .....G.TC.TGGCA .GGGATGGG.  
 N29508 TCTCTGGGAG GTAGGACGGC TGCTTCA TG G.TC.TGGCA .GGGATGGG.  
 N26919 .....  
 N26910 .....  
 H16757 .....G.TC.TGGCA .GGGATGGG.  
 N27732 .....GGCTG GGTCTGNCNA AGGNATGGG

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## Figure 4C (Con't)

1351 1400

Bikunin TTTG CTTTG G AAATCCTC T AGGAGGCT CCTCCT CGC ATGG CC TG  
 R73968 TTTG.CTTTG GGAAATCCTC TTNGGAGGCT CCTCCTCGC ATGGGCCTTG  
 H39840 TTTG.CTTTG GAGAATCCTC T.ANGAGGCT CCTCCT.CGC ATGG.CC.TG  
 H95233 TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG  
 H39841 TTTG.CTTTG G.AAANCNC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG  
 N30199 TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCTCGC ATGG.CC.TG  
 T52966 TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG  
 N29508 TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG  
 N26919 .....GAGGCT CCTCCT.CGC ATGG.CC.TG  
 N26910 .....CTTTT GNAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG  
 H16757 TTTGCCTTTG G.AAANCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG  
 N27732 TTTG.CTTTG G.AAATCCTC TTAGGAGGCT CCTCCT.CGC ATGG.CC.TG

1401 1450

Bikunin CAGT CT GG CAGCAG CCC CGAGTTGTTT CC TCGCTG ATC GATTTC  
 R73968 CAGT.CTNGG CAGCANCCCC CGAGTTTTTT TCGCTCGCTG ATCCGATTTC  
 H39840 CAGT.CT.GG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC  
 H95233 CAGTTCT..G CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC  
 H39841 CAGT.CT.GG CAGCAG.CCC CGAGTTGTTN .CC.TCGCTG ATC.GATNTC  
 N30199 CAGT.CT.GG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC  
 T52966 CAGT.CT.GG CAGCAG..CC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC  
 N29508 CAGT.CT..G CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC  
 N26919 CAGT.CTTGG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ANC.GATTTC  
 N26910 CAGT.CT..G CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATCGGATTTC  
 H16757 CAGTNC.T.GG CAGCAGACCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC  
 N27732 CAGT.CT.GG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ANC.GATTTC

1451 1500

Bikunin TTT CCTCCA GGTAG AGT TTTC TTTC CITATGTTGA ATTCCATTGC  
 R73968 TTTTCTTCCA GGTAAGAATT TTCTTTT  
 H39840 TTT.CCTCCA GGTAG..AGT TTTC.TTTC. CITATGTTGA ATTCCATTGC  
 H95233 TTT.CCTCCA GGTAG..AGT TTTC.TTTC. CITATGTTGA ATTCCATTGC  
 H39841 TTT.CCTCCA GGTAG..AGT TTTC.TTTC. CITATGTTGA ANTCCATTGC  
 N30199 TTT.CCTCCA GGTAG..AGT TTTC.TTTC. CITATGTTGA ATTCCATTGC  
 T52966 TTT.CCTCCA GGTAG..AGT TTTC.TTTC. CITATGTTGA ATTCCATTGC  
 N29508 TTT.CCTCCA GGTAG..AGT TTTC.TTTC. CITATGTTGA ATTCCATTGC  
 N26919 TTT.CCNCCA GGTAG..AGT TTTC.TTTC. CITATGTTGA ATTCCATTGC  
 N26910 TTT.CCTCCA GGTAG..AGT TTTC.TTTC. CITATGTTGA ATTCCATTGC  
 H16757 TTTACCCCA GGTAG..AGT TTTCCTTTCN CITATGTTGA ATTCCATTGC  
 N27732 TTT.CCTCCA GGTAG..AGT TTTC.TTTC. CITATGTTGA ATTCCATTGC

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Figur 4C (Con't)

1501 1550  
 Bikunin CTCTTTT CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT GT  
 H39840 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTTGT  
 H95233 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT  
 H39841 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT  
 N30199 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT  
 T52966 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT  
 N29508 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT  
 N26919 CTCTTTT.CN CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT  
 N26910 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT  
 H16757 CTCTTTTACT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT  
 N27732 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT

1551 1600  
 Bikunin CTGATTATG G TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT  
 H39840 CTGATTATG GGTTTTTTT AAGTAT  
 H95233 CTGATTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT  
 H39841 CTGATTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT  
 N30199 CTGATTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT  
 T52966 CTGATTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT  
 N29508 CTGATTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT  
 N26919 CTGATTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT  
 N26910 CTGATTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT  
 H16757 CTGATTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT  
 N27732 CTGATTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT

1601 1650  
 Bikunin CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC  
 H95233 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAA  
 H39841 CTGAAAGAAG GAAAGTAAAN TGTACAAGTT TAATAAAAAG GGGCCTTCCC  
 N30199 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC  
 T52966 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC  
 N29508 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC  
 N26919 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC  
 N26910 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC  
 H16757 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC  
 N27732 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC

1651 1689  
 Bikunin CTTTAG AAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA  
 H39841 CTTTAA.  
 N30199 CTTTAG.AAT AAA  
 T52966 CTTTAGGAAT NAAAAA AAAAGGTC  
 N29508 CTTTAG.AAT AAATTCAGC ATGTGCTTTC AA  
 N26919 CTTTAG.AAT AAAAAAAAAA AAAAAAAAAA A  
 N26910 CTTTAG.AAT AAATTCAGC ATGTGCTTTC AAAAAA  
 H16757 CTTTAG.AAT AAAAAAAAAA AAAAAAAAAA AAAAAA  
 N27732 CTTTAG.AAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

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FIGURE 4D

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EST c nsens MLRAEADGVS RLLGSLLLSG VLAADRERSI HDFCLVSKVV GRCRASMPRW 50  
EST consens WYNVTDGSCQ LFVYGGCDGN SNNYLTKEEC LKKCATVTEN ATGDLATSRN 100  
EST consens AADSSVPSAP RRQSEDHSS DMFNYEEYCT ANAVTGPCRA SFPRWYFDVE 150  
EST consens RNSCWNFIYG GCRGNKNSYR SEEACMLRCF RQENPPLPL GSKVVVLAGL 200  
EST consens FVMVLLFLG ASMYLIRVA RRNQERALRT VWSSGDDKEQ LVKNTYVL 248

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FIGURE 4E

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cDNA ACC 3  
 translation T -47

cDNA TGATCGCGAG ACCCCAACGG CTGGTGGCGT CGCCTGCGCG TCTCGGCTGA 53  
 translation . S R D P N G W W R R L R V S A E -30

cDNA GCTGGCCATG GCGCAGCTGT GCGGGCTGAG GCGGAGCCGG GCGTTTCTCG 103  
 translation L A M A Q L C G L R R S R A F L A-13

cDNA CCCTGCTGGG ATCGCTGCTC CTCTCTGGGG TCCTGGCGGC CGACCGAGAA 153  
 translation L L G S L L L S G V L A A D R E 4

cDNA CGCAGCATCC ACGACTTCTG CCTGGTGTCTG AAGGTGGTGG GCAGATGCCG 203  
 translation R S I H D F C L V S K V V G R C R 21

cDNA GGCCTCCATG CCTAGGTGGT GGTACAATGT CACTGACGGA TCCTGCCAGC 253  
 translation A S M P R W W Y N V T D G S C Q L 38

cDNA TGTTTGTGTA TGGGGGCTGT GACGGAAACA GCAATAATTA CCTGACCAAG 303  
 translation F V Y G G C D G N S N N Y L T K 54

cDNA GAGGAGTGCC TCAAGAAATG TGCCACTGTC ACAGAGAATG CCACGGGTGA 353  
 translation E E C L K K C A T V T E N A T G D 71

cDNA CCTGGCCACC AGCAGGAATG CAGCGGATTC CTCTGTCCCA AGTGCTCCCA 403  
 translation L A T S R N A A D S S V P S A P R 88

cDNA GAAGGCAGGA TTCTGAAGAC CACTCCAGCG ATATGTTCAA CTATGAAGAA 453  
 translation R Q D S E D H S S D M F N Y E E 104

cDNA TACTGCACCG CCAACGCAGT CACTGGGCCT TGCCGTGCAT CCTTCCCACG 503  
 translation Y C T A N A V T G P C R A S F P R 121

cDNA CTGGTACTTT GACGTGGAGA GGAACCTCTG CAATAACTTC ATCTATGGAG 553  
 translation W Y F D V E R N S C N N F I Y G G 138

cDNA GCTGCCGGGG CAATAAGAAC AGCTACCGCT CTGAGGAGGC CTGCATGCTC 603  
 translation C R G N K N S Y R S E E A C M L 154

cDNA CGCTGCTTCC GCCAGCAGGA GAATCCTCCC CTGCCCCTTG GCTCAAAGGT 653  
 translation R C F R Q Q E N P P L P L G S K Y 171

cDNA GGTGGTTCTG GCGGGGCTGT TCGTGATGGT GTTGATCCTC TTCCTGGGAG 703  
 translation V V L A G L F V M V L I L F L G A 198

cDNA CCTCCATGGT CTACCTGATC CGGGTGGCAC GGAGGAACCA GGAGCGTGCC 753  
 translation S M V Y L I R V A R R N Q E R A 204

cDNA CTGCGCACCG TCTGGAGCTT CGGAGATGA 792  
 translation L R T V W S F G D 213

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FIGURE 4F

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cDNA GCACGAGTTG GGAGGTGTAG CGCGGCTCTG AACGCGCTGA GGGCCGTTGA 50  
 cDNA GTGTGCGCAGG CGGCGAGGGC GCGAGTGAGG AGCAGACCCA GGCATCGCGC 100  
 cDNA GCCGAGAAGG CCGGGCGTCC CCACACTGAA GGTCCGGAAG GGCAGCTTCC 150  
 cDNA GGGGGCTTTG GCACCTGGCG GACCCTCCCG GAGCGTCGGC ACCTGAACGC 200  
 cDNA GAGGCGCTCC ATTGCGCGTG CGCGTTGAGG GGCTTCCCGC ACCTGATCGC 250  
 cDNA GAGACCCCA CGGCTGGTGG CGTCGCCTGC GCGTCTCGGC TGAGCTGGCC 300  
 cDNA ATGGCGCAGC TGTGCGGGCT GAGGCGGAGC CGGGCGTTTC TCGCCCTGCT 350  
 translation M A Q L C G L R R S R A F L A L L -11

cDNA GGGATCGCTG CTCCTCTCTG GGGTCCTGGC GGCCGACCGA GAACGCAGCA 400  
 translation G S L L L S G V L A A D R E R S I 7

cDNA TCCACGACTT CTGCCTGGTG TCGAAGGTGG TGGGCAGATG CCGGGCCTCC 450  
 translation H D F C L V S K V V G R C R A S 23

cDNA ATGCCTAGGT GGTGGTACAA TGTCCTGAC GGATCCTGCC AGCTGTTTGT 500  
 translation M P R W W Y N V T D G S C Q L F V 40

cDNA GTATGGGGGC TGTGACGGAA ACAGCAATAA TTACCTGACC AAGGAGGAGT 550  
 translation Y G G C D G N S N N Y L T K E E C 57

cDNA GCCTCAAGAA ATGTGCCACT GTCACAGAGA ATGCCACGGG TGACCTGGCC 600  
 translation L K K C A T V T E N A T G D L A 73

cDNA ACCAGCAGGA ATGCAGCGGA TTCCTCTGTC CCAAGTGCTC CCAGAAGGCA 650  
 translation T S R N A A D S S V P S A P R R Q 90

cDNA GGATTCTGAA GACCACTCCA GCGATATGTT CAACTATGAA GAATACTGCA 700  
 translation D S E D H S S D M F N Y E E Y C T 107

cDNA CCGCCAACGC AGTCACTGGG CTTTGCCGTG CATCCTTCCC ACGCTGGTAC 750  
 translation A N A V T G P C R A S F P R W Y 123

cDNA TTTGACGTGG AGAGGAACTC CTGCAATAAC TTCATCTATG GAGGCTGCCG 800  
 translation F D V E R N S C N N F I Y G G C R 140

cDNA GGGCAATAAG AACAGCTACC GCTCTGAGGA GGCCTGCATG CTCCGCTGCT 850  
 translation G N K N S Y R S E E A C M L R C F 157

cDNA TCCGCCAGCA GGAGAATCCT CCCCTGCCCC TTGGCTCAAA GGTGGTGGTT 900  
 translation R Q Q E N P P L P L G S K V V V 173

cDNA CTGGCGGGGC TGTTCTGTAT GGTGTTGATC CTCTTCCTGG GAGCCTCCAT 950  
 translation L A G L F V M V L L L F L G A S M 190

cDNA GGTCTACCTG ATCCGGGTGG CACGGAGGAA CCAGGAGCGT GCCCTGCGCA 1000  
 translation V Y L I R V A R R N Q E R A L R T 207

cDNA CCGTCTGGAG CTCCGGAGAT GACAAGGAGC AGCTGGTGAA GAACACATAT 1050  
 translation V W S S G D D K E Q L V K N T Y 223

cDNA GTCCTGTGAC CGCCCTGTCT CCAAGAGGAC TGGGGAAGGG AGGGGAGACT 1100  
 translation V L \* 225

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FIGURE 4F (Con't)

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cDNA	ATGTGTGAGC	TTTTTTTAAA	TAGAGGGATT	GACTCGGATT	TGAGTGATCA	1150
cDNA	TTAGGGCTGA	GGTCTGTTTC	TCTGGGAGGT	AGGACGGCTG	CTTCCTGGTC	1200
cDNA	TGGCAGGGAT	GGGTTTGCTT	TGGAAATCCT	CTAGGAGGCT	CCTCCTCGCA	1250
cDNA	TGGCCTGCAG	TCTGGCAGCA	GCCCCGAGTT	GTTTCCTCGC	TGATCGATTT	1300
cDNA	CTTTCCTCCA	GGTAGAGTTT	TCTTTGCTTA	TGTTGAATTC	CATTGCCTCC	1350
cDNA	TTTTCTCNAT	CACAGAAGTG	ATGTTGGAAT	CGTTTCTTTT	GTTTGTCTGA	1400
cDNA	TTTATGGTTT	TTTTAAGTAT	AAACAAAAGT	TTTTTATTAG	CATTCTGAAA	1450
cDNA	GAAGGAAAGT	AAAATGTACA	AGTTTAATAA	AAAGGGGCCT	TCCCCTTTAG	1500
cDNA	AATAAATTTT	CAGCATGTTG	CTTTCAAAAA	AAAAAAAAAA	AAAA	

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**SECRET**

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# Purification of Placental Bikunin using Superdex 75 Gel-Filtration

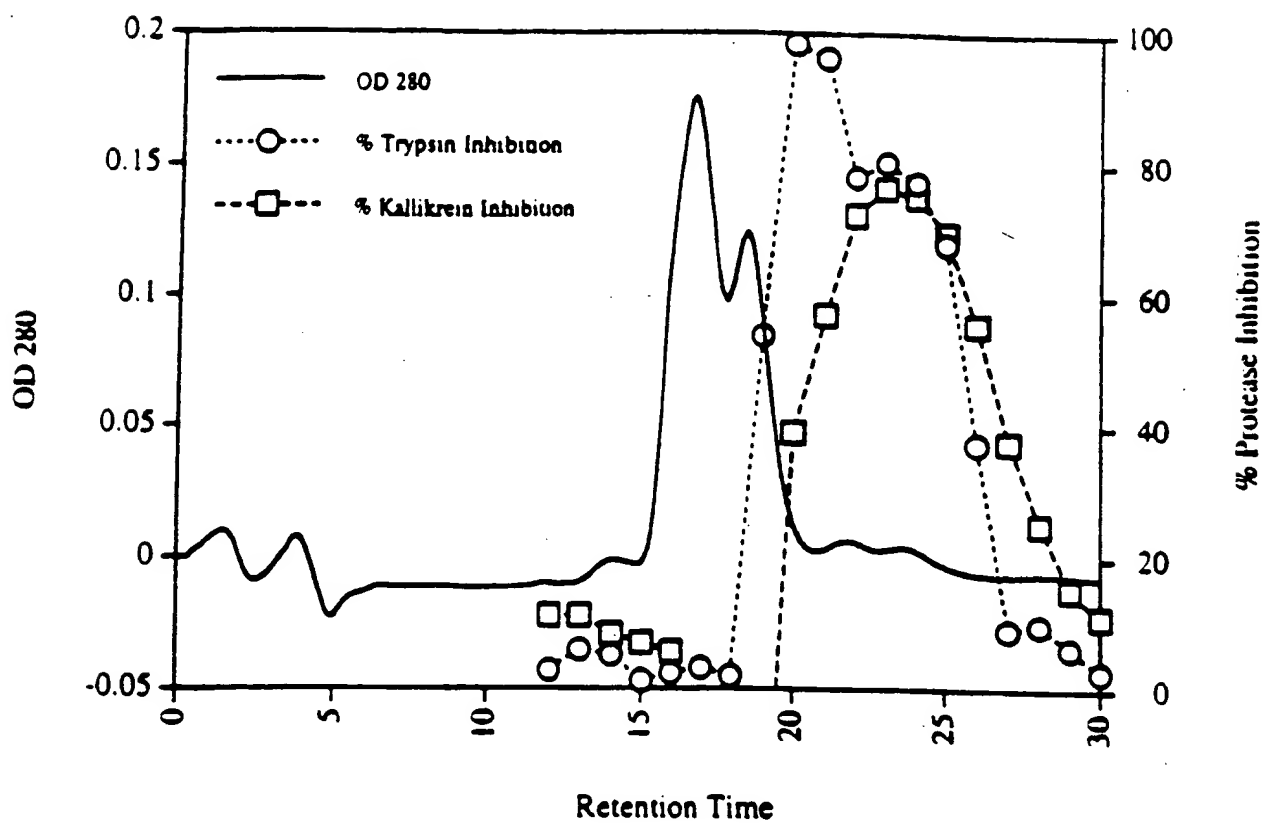


FIGURE 5



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OD 215

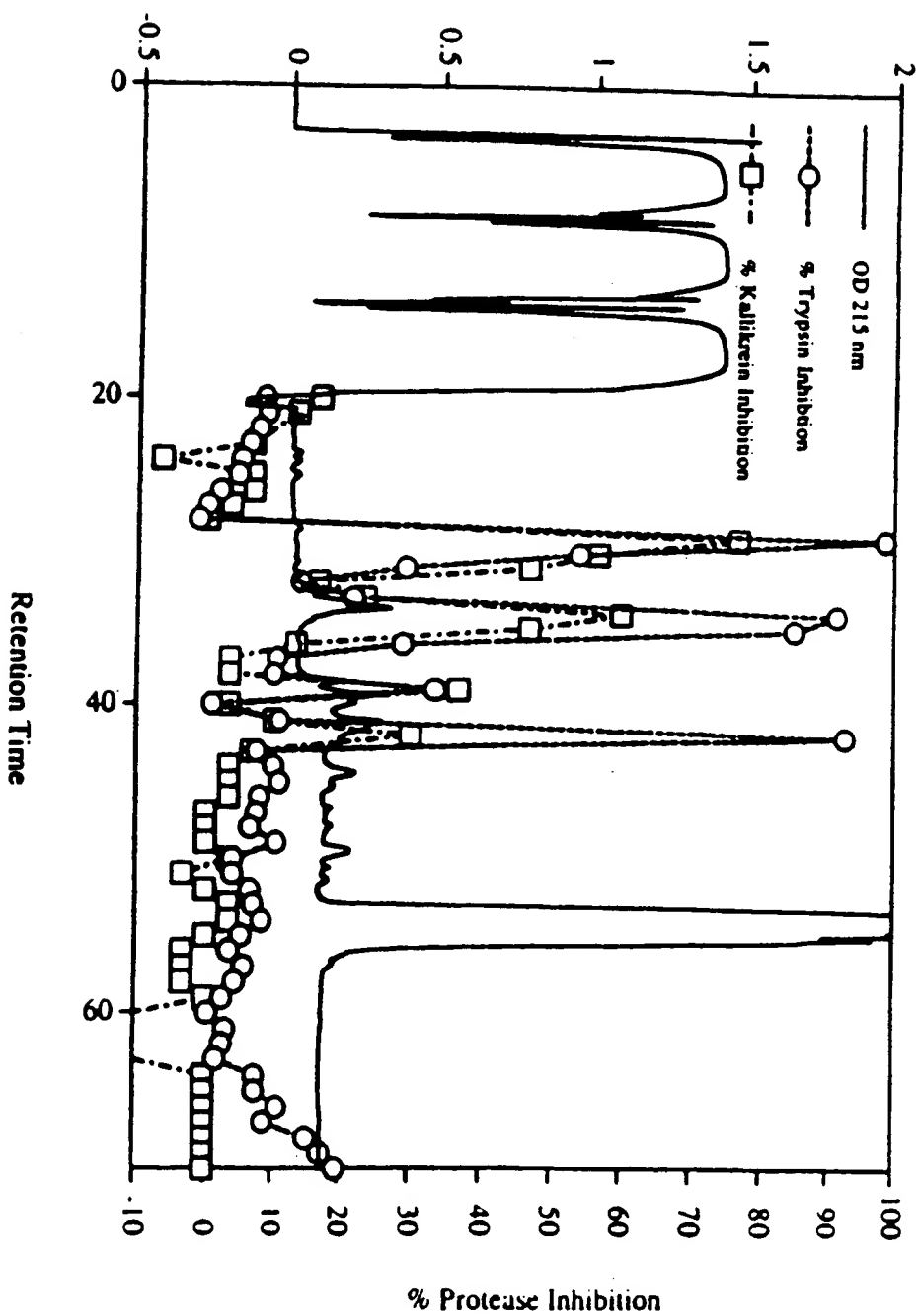


FIGURE 6

Purification of Placental Bikunin using C18 Reverse-Phase Chromatography

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**Figure 7**

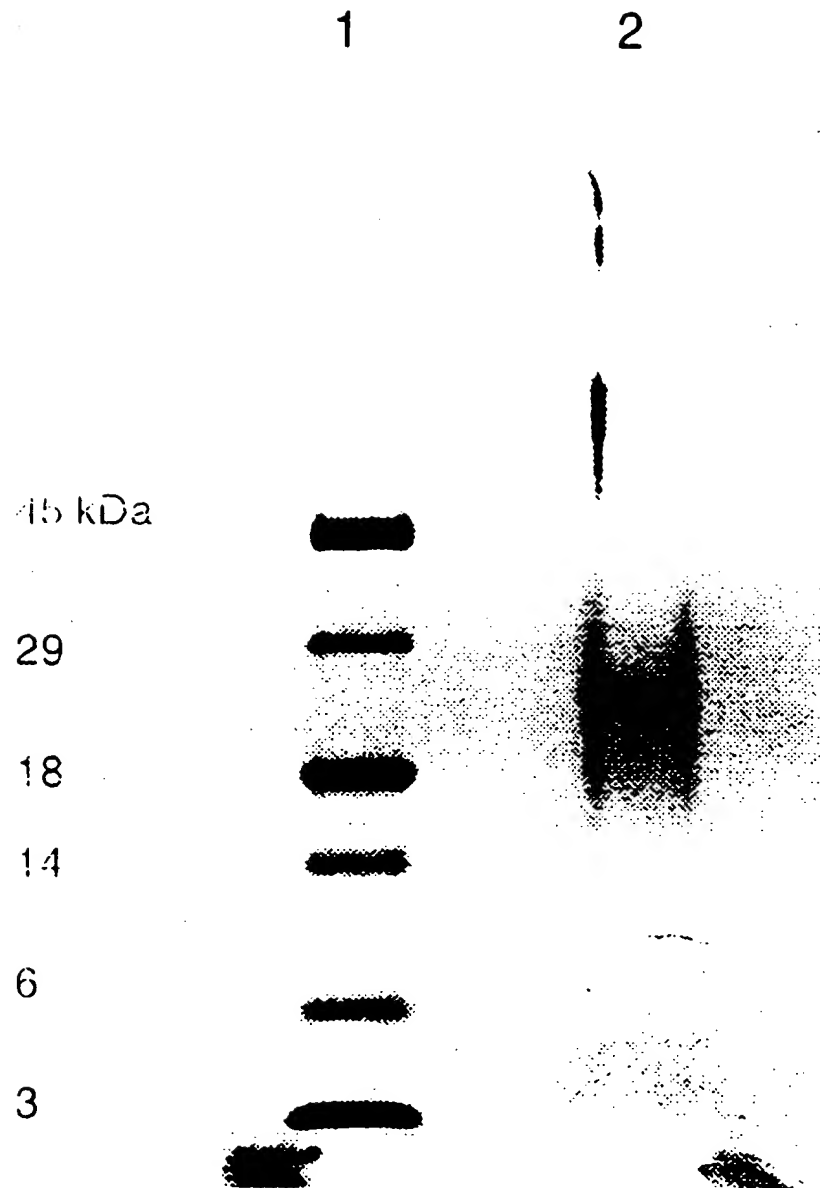


Figure 8A

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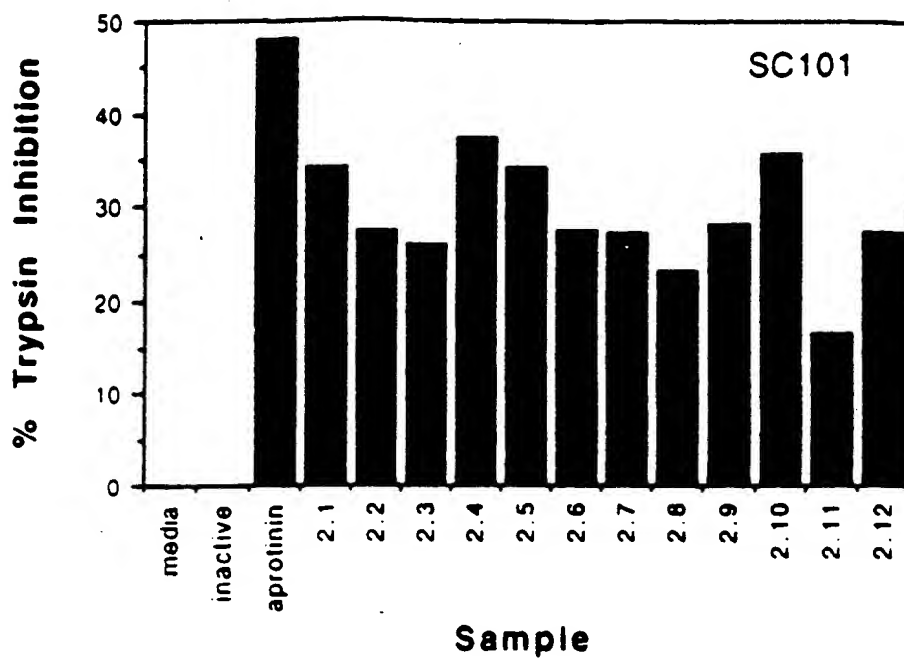
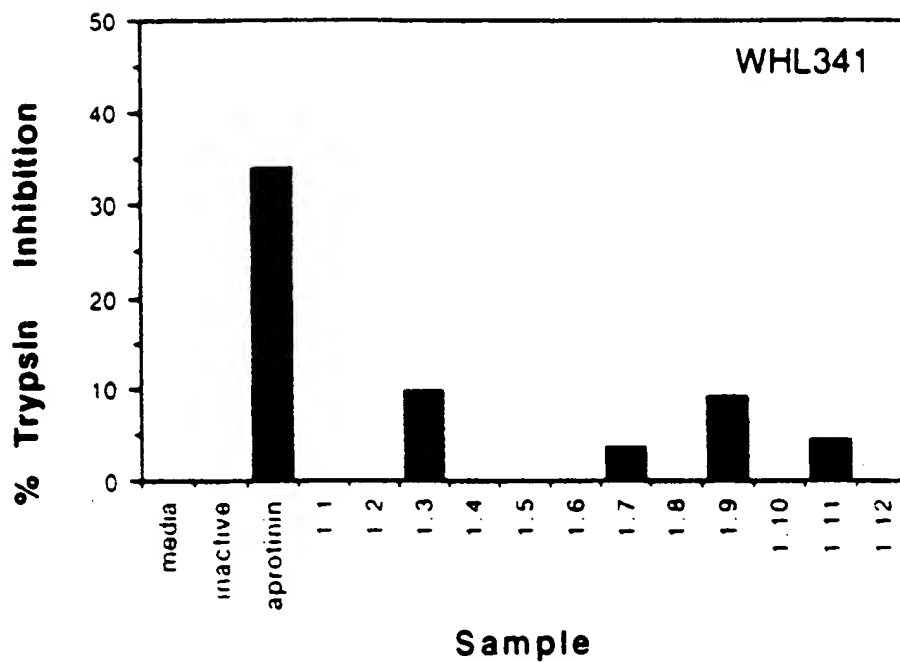


Figure 8B



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Figure 9A

SDS-PAGE

Aprotinin  
2.4  
2.5

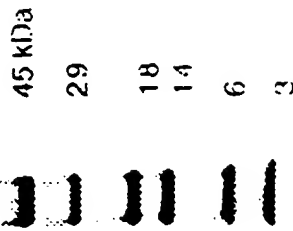
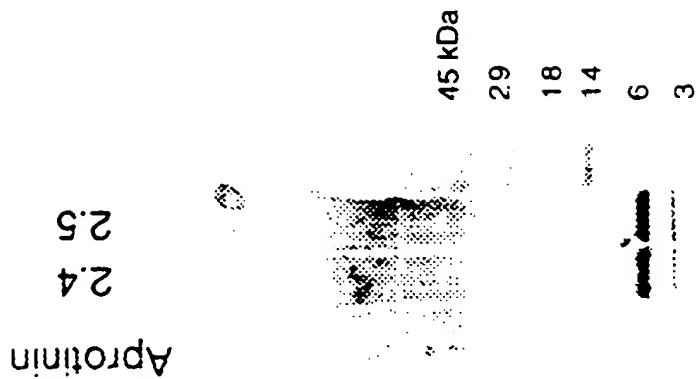


Figure 9B

Western



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Figure 10

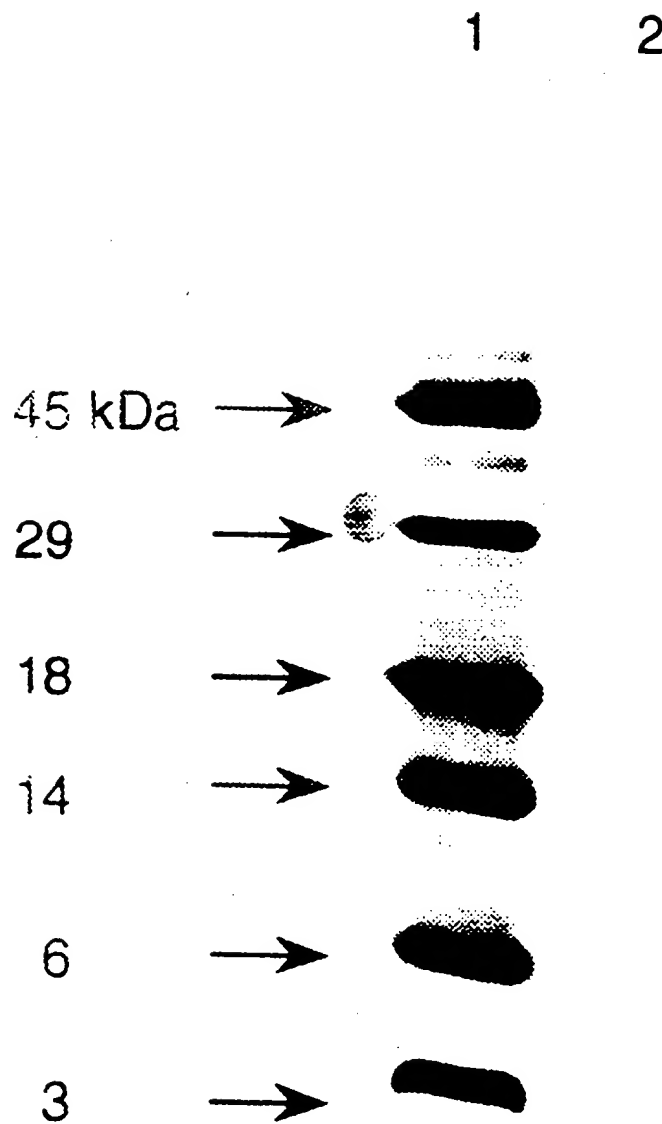


Figure 11A

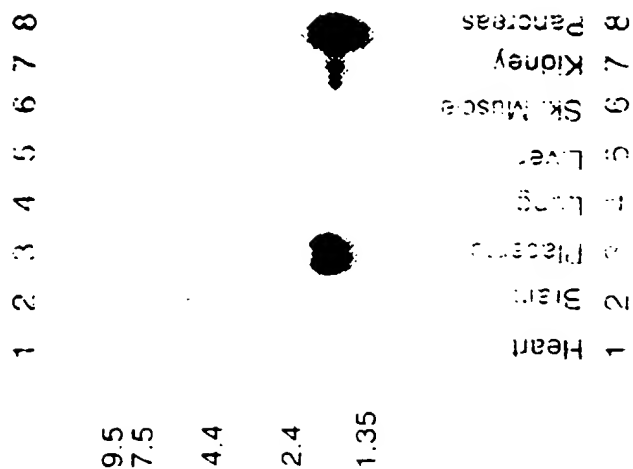
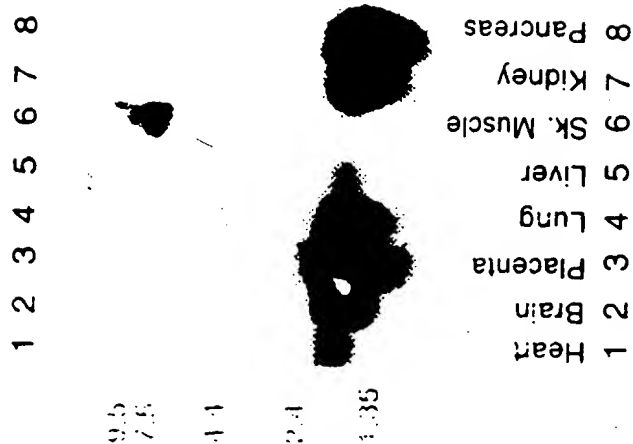


Figure 11B



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Figure 12A

1 2 3 4

45 kDa  
29  
18  
14  
6  
3



Figure 12B

1 2 3 4

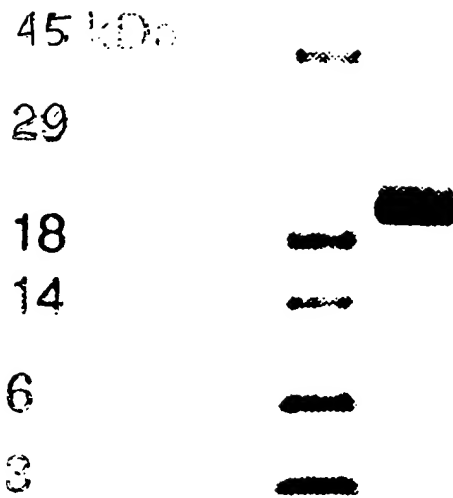
45 kDa  
29  
18  
14  
6  
3



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Figure 13

1 2

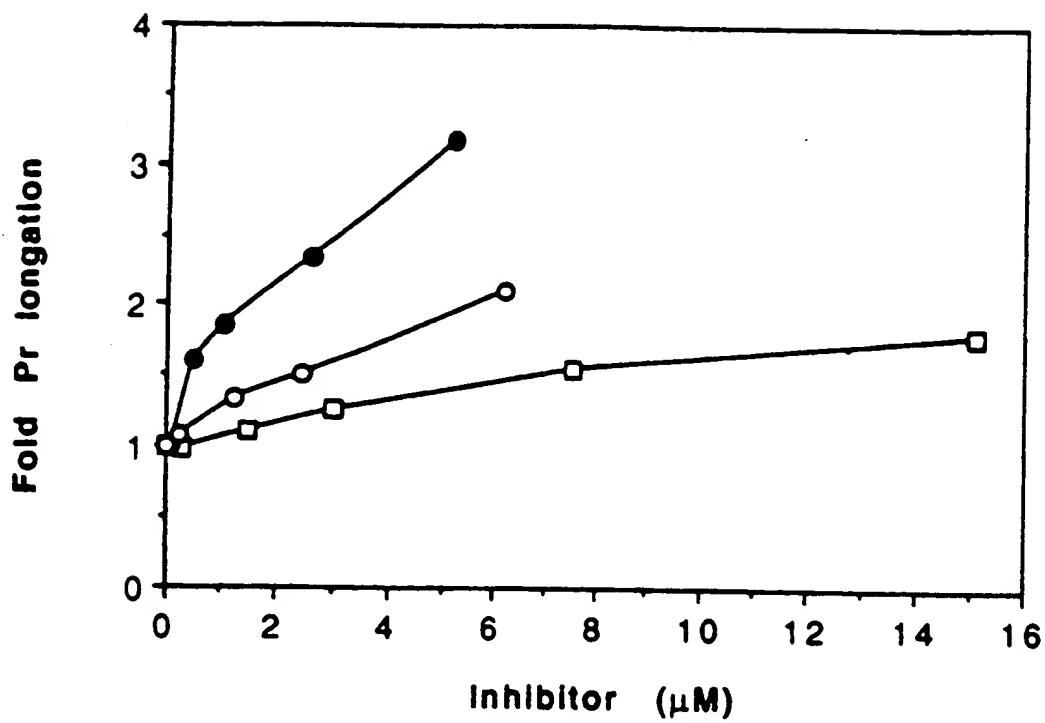


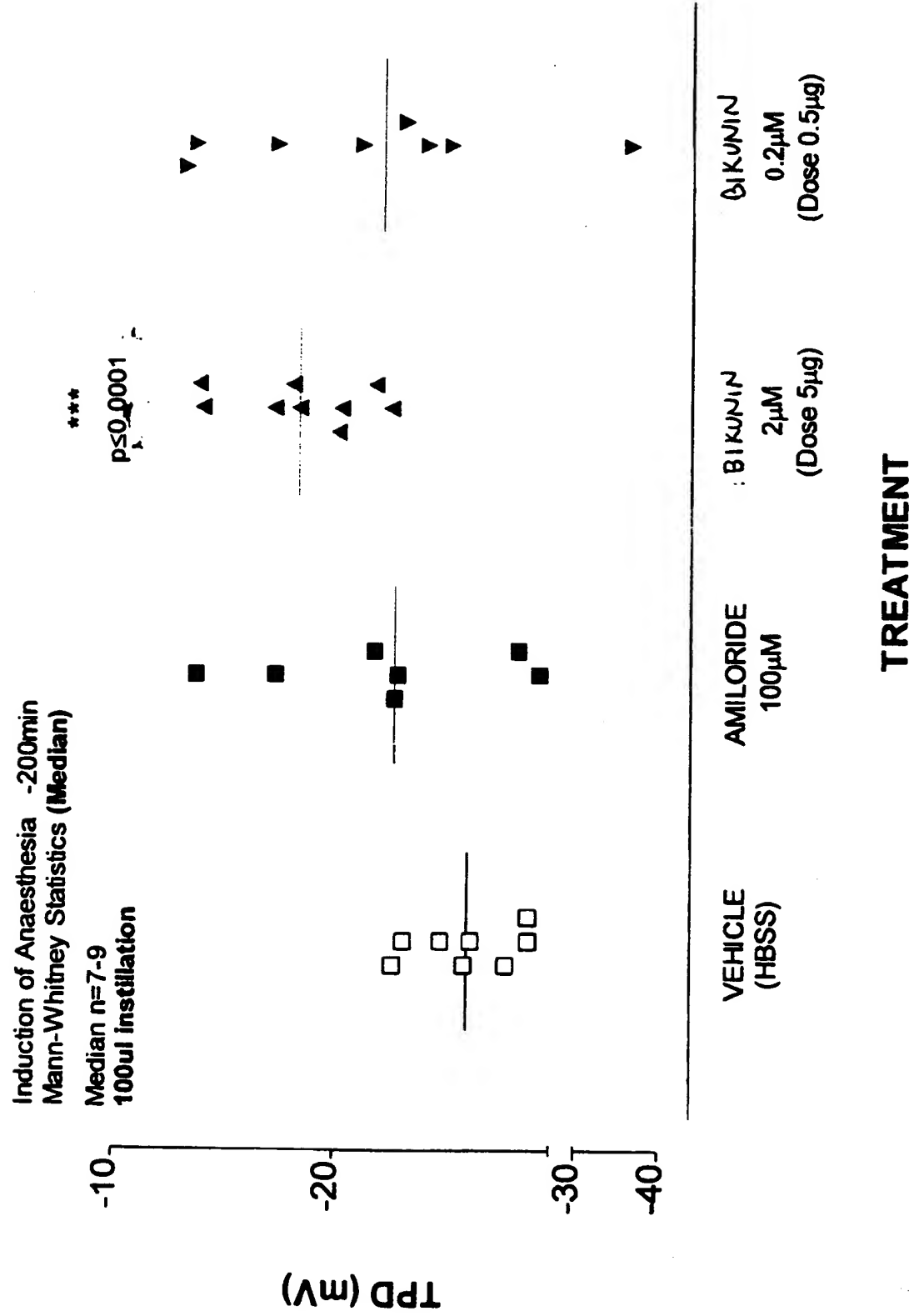
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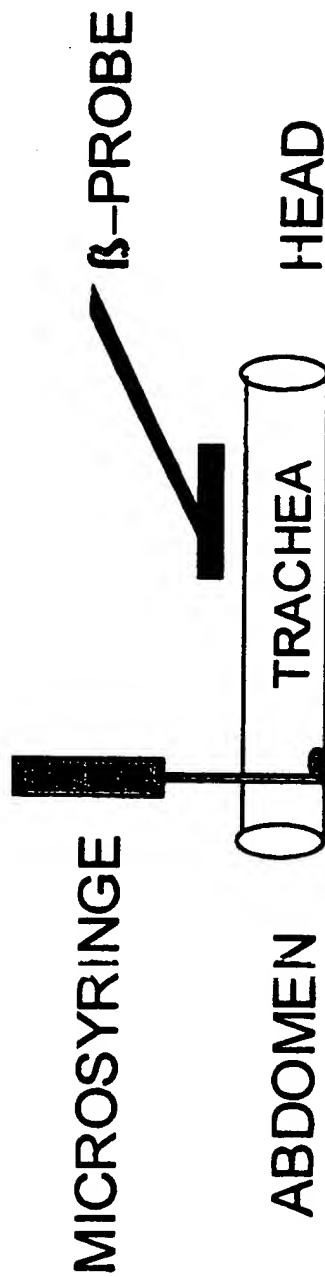
Figure 14





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Figure 16 (a) : Diagram to show the arrangement of needle and Beta probe.



Longitudinal view

Figure 16 (b) : Counts detected by the probe as the  $^{32}\text{P}$ -labeled Saccharomyces cerevisiae are transported along the tracheal mucociliary layer.

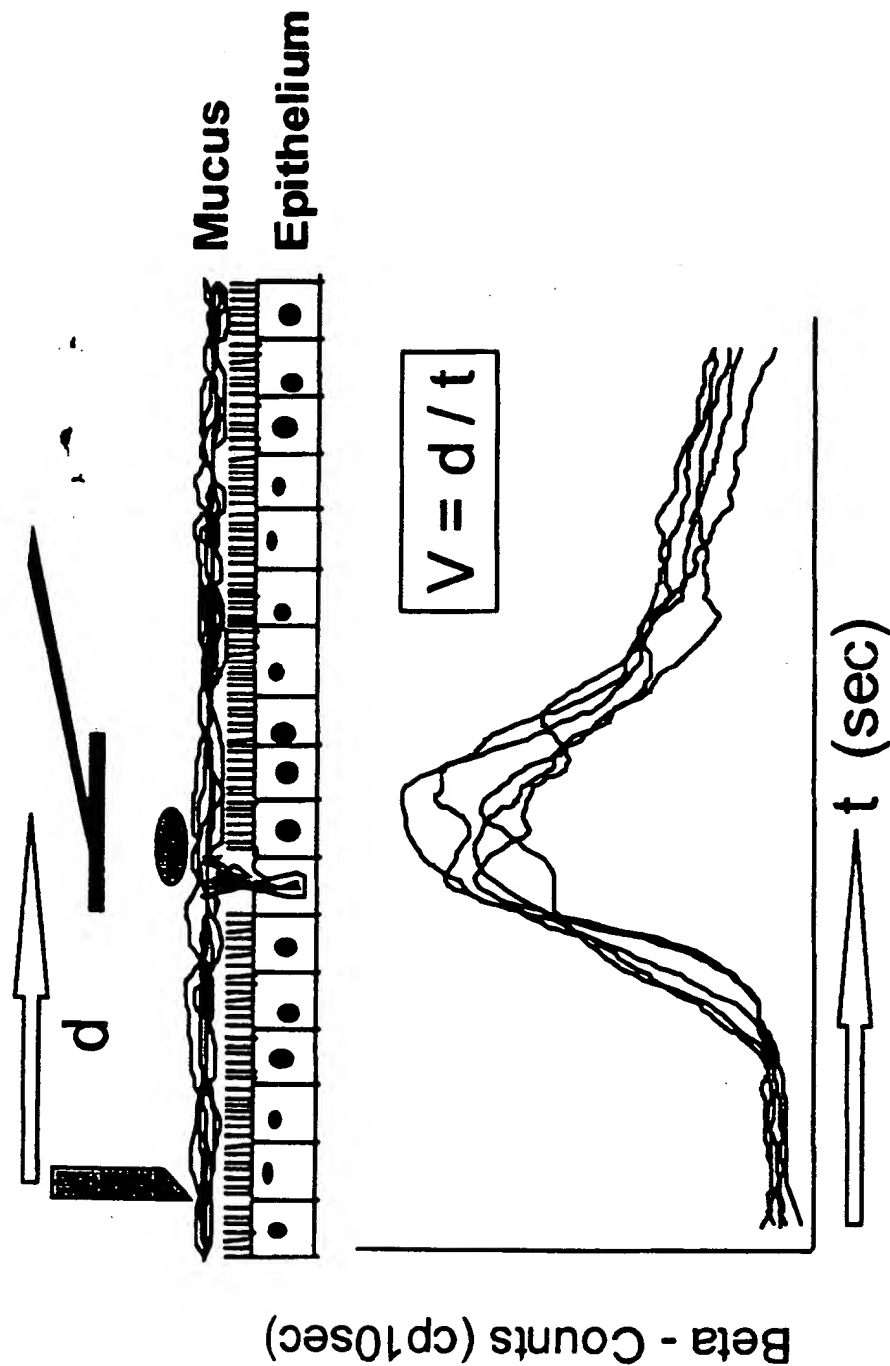


Figure 17 : Short circuit current (Isc) trace to show the action of  $\beta$ IKUNIN (70nM) on sodium dependent current in cultured normal human bronchial epithelial cells in vitro

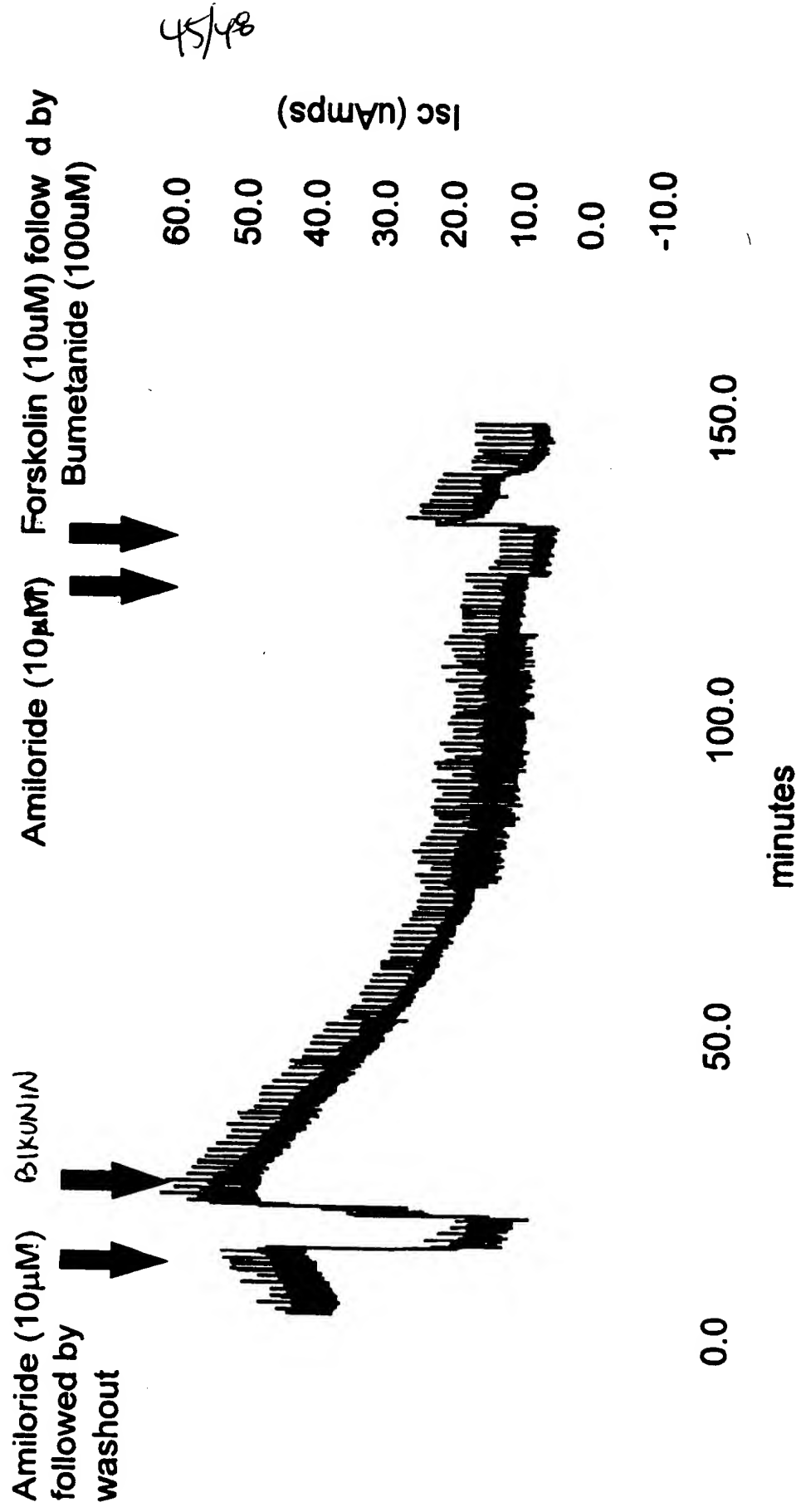


Figure 18 : The effect of a 5 min aerosol of hypertonic saline (14.4%) on tracheal mucus velocity (TMV) in the anaesthetised spontaneously breathing guinea-pig

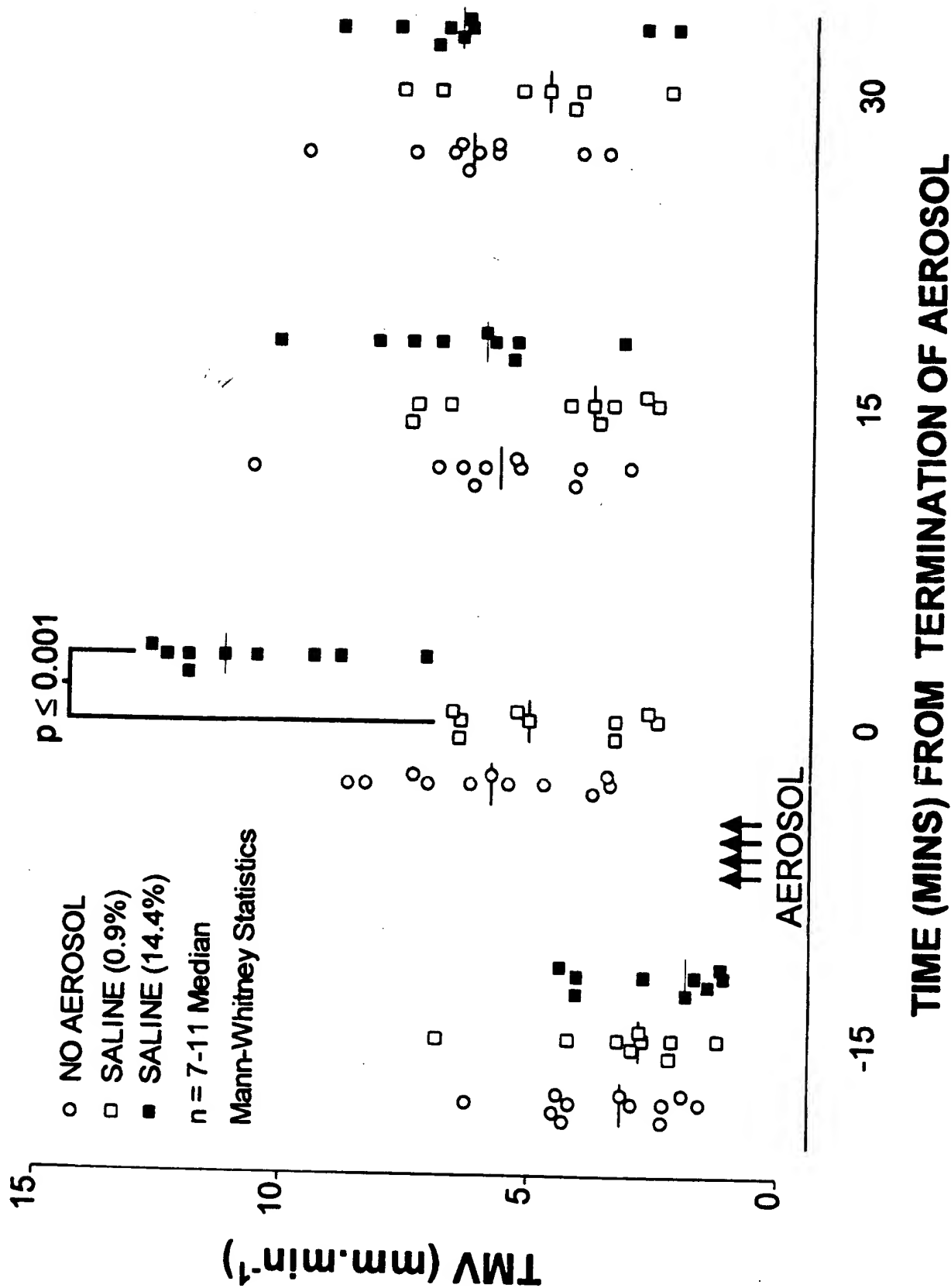
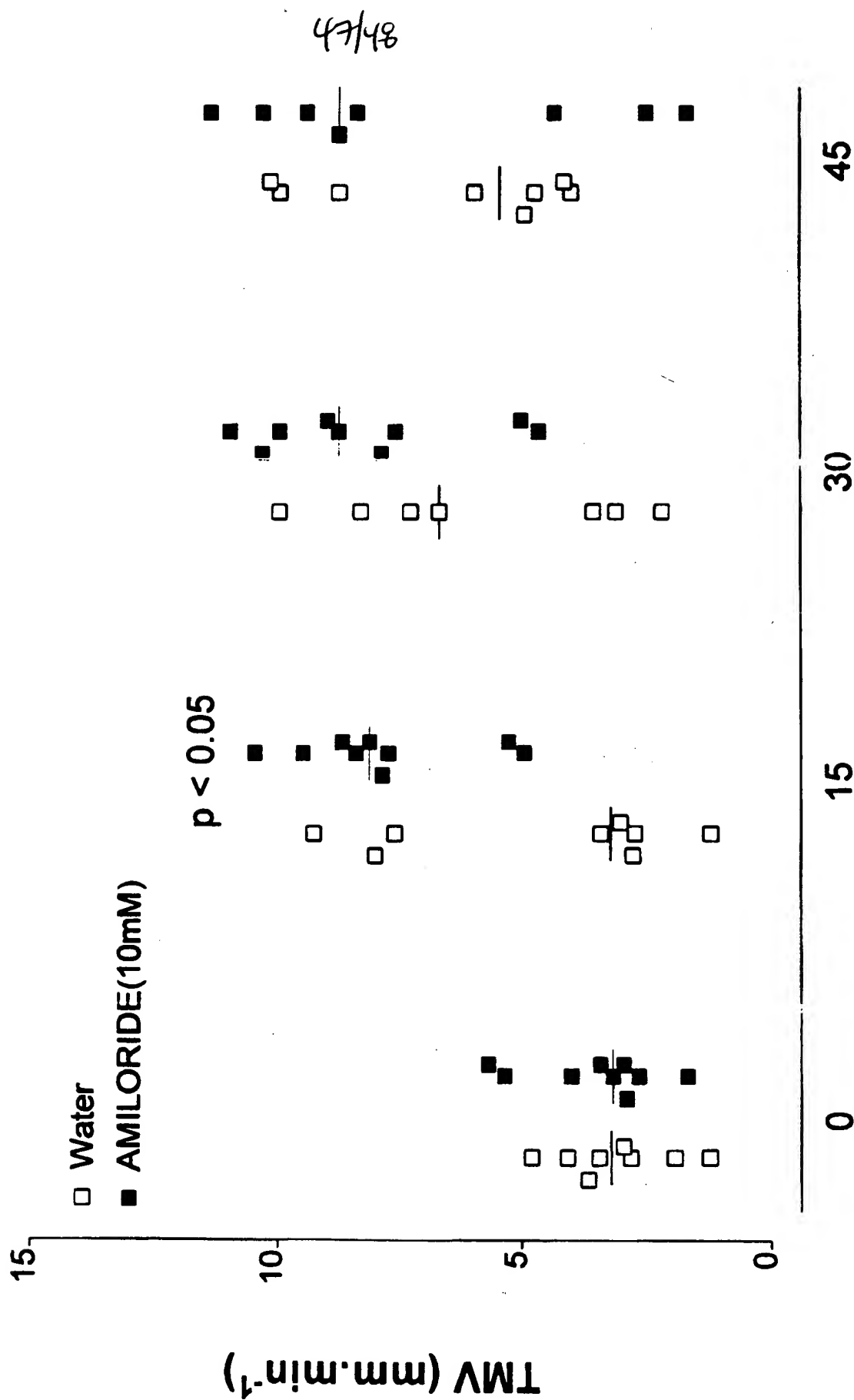


Figure 19 : The effect of a 20 min aerosol of amiloride (10mM) on tracheal mucus velocity (TMV) in the anaesthetised spontaneously breathing guinea-pig



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Figure 20 : Short circuit current (Isc) trace to show the action of Aprotinin Double  
mucin (0.5-5ug.ml<sup>-1</sup>) on sodium dependent current in normal human  
bronchial epithelial cells in vitro

